



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 145765

TO: Terry McKelvey
Location: REM-2A75&2C70
Art Unit: 1636
Saturday, March 05, 2005
Case Serial Number: 10/006116

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner McKelvey,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527



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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2005, 18:06:39 ; Search time 41 Seconds
(without alignments)
581.994 Million cell updates/sec

Title: US-10-006-116A-194

Perfect score: 1374

Sequence: 1 MGSLIFLLCLVGLGSQLP.....GVYTYICKYVDIMIRNN 248

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79: *
1: P1r1: *
2: P1r2: *
3: P1r3: *
4: P1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.5	45.3	260	2	156559
2	569.5	41.4	248	2	S55066
3	567	41.3	248	2	S55067
4	561	40.8	231	1	TRPGTR
5	555	40.4	243	2	A35871
6	555	40.4	253	2	A53968
7	553	40.2	246	2	B25528
8	552	40.2	229	1	TRBQTR
9	550	40.0	247	2	S13813
10	546	39.7	247	1	TRDG
11	545	39.6	246	1	TRDGC
12	544.5	39.6	247	2	A27547
13	543	39.5	246	1	TRRT1
14	540	39.3	238	2	S31779
15	533.5	38.8	247	2	S05494
16	532	38.7	246	1	TRRT2
17	527.5	38.4	261	2	A31136
18	524	38.1	232	1	KQPG
19	520.5	37.9	261	2	A25606
20	519	37.8	246	2	JQ1471
21	518	37.7	246	2	JQ1472
22	518	37.7	261	2	A34079
23	513.5	37.4	231	2	S31778
24	513.5	37.4	239	2	A27207
25	511.5	37.2	261	2	S45303
26	510.5	37.2	261	1	NGMSG
27	508	37.0	242	2	S31776
28	508	37.0	242	2	S31775
29	503	36.6	260	2	A37938

30	503	36.6	263	2	S15686	tissue kallikrein
31	502	36.5	259	2	B31136	tissue kallikrein
32	501	36.5	247	1	B25852	trypsin (EC 3.4.21
33	499.5	36.4	241	2	S39048	trypsin (EC 3.4.21
34	496.5	36.1	261	1	TRMSM5	tissue kallikrein
35	496	36.1	242	2	S49489	trypsin (EC 3.4.21
36	495.5	36.1	257	2	S33772	tissue kallikrein
37	495.5	36.1	261	2	S01971	tissue kallikrein
38	494.5	36.0	247	1	A25852	trypsin (EC 3.4.21
39	493	35.9	262	1	KQHU	tissue kallikrein
40	491.5	35.8	240	2	S39047	trypsin (EC 3.4.21
41	491	35.7	256	1	NGMSA	7S nerve growth fa
42	490.5	35.7	229	1	TRDFS	trypsin (EC 3.4.21
43	490.5	35.7	261	2	A41020	tissue kallikrein
44	489	35.6	244	2	A44284	tissue kallikrein
45	485.5	35.3	261	2	J50236	tissue kallikrein
46	484.5	35.3	259	2	A29746	tissue kallikrein
47	484.5	35.3	304	2	S33496	trypsin (EC 3.4.21
48	483.5	35.2	265	1	KQRTF	tissue kallikrein
49	481.5	35.0	250	2	T01779	trypsin (EC 3.4.21
50	481.5	35.0	261	2	A29745	tissue kallikrein
51	479	34.9	261	1	S35711	semenogelase (EC 3
52	477.5	34.8	261	1	KQMS1	tissue kallikrein
53	476	34.6	259	2	I18363	trypsin (EC 3.4.21
54	470.5	34.2	261	1	A32297	semenogelase (EC 3
55	469.5	34.2	261	2	A24378	tissue kallikrein
56	468	34.1	259	1	KQRTN	tissue kallikrein
57	467.5	34.0	261	1	BQMSB	tonin (EC 3.4.21.-
58	467	34.0	247	2	S12764	tissue kallikrein
59	461.5	33.6	259	2	D23863	trypsin (EC 3.4.21
60	458.5	33.4	250	2	S31384	tissue kallikrein
61	458.5	33.4	261	2	A29586	trypsin (EC 3.4.21
62	449	32.7	258	2	A57280	tissue kallikrein
63	436.5	31.8	257	2	S15685	venom plasminogen
64	436.5	31.8	250	1	JC2479	kallikrein, glandu
65	432	31.4	236	1	A32121	venomom B (EC 3.4
66	431.5	31.4	261	2	A28062	snake venom factor
67	431	31.4	262	1	JC4803	gamma-remun (EC 3
68	422.5	30.7	233	1	UC0169	venomom A (EC 3.4
69	417	30.3	236	1	B32121	venomom A (EC 3.4
70	411.5	29.9	228	1	S35689	snake venom factor
71	408	29.7	235	1	S65621	venomom AB (EC 3
72	406.5	29.6	231	2	A60468	venomom A (EC 3.4
73	402	29.3	255	1	A28169	venomom A (EC 3.4
74	394	28.7	236	1	A41456	venomom A (EC 3.4
75	388	28.2	269	2	A26823	pancreatic elastase
76	386	28.1	232	1	A54361	venomom A (EC 3.4
77	385.5	28.1	188	2	B32340	tissue kallikrein
78	385.5	28.1	264	2	I18136	chymotrypsin-like
79	382.5	27.8	1524	2	T30337	polypotein - Afri
80	382	27.8	246	1	DBHU	complement factor
81	381	27.7	263	1	I15608	complement factor
82	377	27.4	225	2	S45356	probable serine pr
83	374.5	27.3	259	1	WMMS28	complement factor
84	371	27.0	271	1	ELRT2	pancreatic elastase
85	370.5	27.0	263	2	A21195	chymotrypsin (EC 3
86	370	26.9	234	1	S20407	venomom A (EC 3.4
87	368.5	26.8	638	1	A57014	proctasin (EC 3.4
88	367.5	26.7	638	1	KQHUP	plasma kallikrein
89	366	26.6	258	1	S36783	venomom A (EC 3.4
90	364	26.5	156	2	B33863	tissue kallikrein
91	362.5	26.4	246	2	S64707	chymase (EC 3.4.21
92	359.5	26.2	247	2	S55340	trypsin (EC 3.4.21
93	359	26.1	443	2	I46932	coagulation factor
94	358	26.1	812	1	PLBO	plasmin (EC 3.4.21
95	357	26.0	261	2	A31372	granzyme A (EC 3.4
96	357	26.0	263	2	A31299	chymotrypsin (EC 3
97	357	26.0	271	2	S29239	chymotrypsin (EC 3
98	357	26.0	1019	2	A38738	coagulation factor
99	355.5	25.9	276	2	A38654	maet cell proteina
100	354	25.8	271	2	A25528	pancreatic elastase
101	353.5	25.7	263	2	S47537	chymotrypsin (EC 3
102	353.5	25.7	270	2	S56160	maet cell tryptase

103	353	25.7	274	2	JC4171	trypase (EC 3.4.2
104	352	25.6	260	1	A45061	granzyme A (EC 3.4
105	352	25.6	461	1	JX0210	protein C (activat
106	351	25.5	456	1	KXBO	protein C (activat
107	349.5	25.4	269	2	B26823	pancreatic elastas
108	348	25.3	267	2	S40006	trypsin (EC 3.4.21
109	347	25.3	461	1	KXHU	protein C (activat
110	346.5	25.2	244	1	S26042	chymase (EC 3.4.21
111	346.5	25.2	461	1	S18994	protein C (activat
112	344	25.0	275	2	B35863	trypsin (EC 3.4.2
113	343.5	25.0	273	2	A47246	trypsin (EC 3.4.2
114	343.5	25.0	274	2	S35339	trypsin (EC 3.4.21
115	343	25.0	275	2	A32410	trypsin (EC 3.4.2
116	342.5	24.9	558	2	JCS878	plasma hyaluronan-
117	342.5	24.9	810	2	PLHU	plasma (EC 3.4.21
118	342	24.9	275	2	C35863	trypsin (EC 3.4.21
119	342	24.9	275	2	A35863	trypsin (EC 3.4.21
120	341.5	24.9	258	2	I56220	trypsin (EC 3.4.2
121	340.5	24.8	246	2	B38678	trypsin (EC 3.4.2
122	339.5	24.7	258	2	A45161	trypsin (EC 3.4.2
123	339.5	24.7	267	4	A56615	trypsin (EC 3.4.2
124	339	24.7	257	2	B45061	trypsin (EC 3.4.2
125	339	24.7	461	1	KFHU	serine proteinase
126	338	24.7	625	1	KFHU1	probable pancreati
127	338	24.6	625	1	TRWV5Y	granzyme A (EC 3.4
128	337.5	24.6	238	2	TRWV5Y	coagulation factor
129	337.5	24.6	264	2	S65663	thrombin (EC 3.4.2
130	337	24.5	434	1	A35005	trypsin-like prote
131	337	24.5	812	1	PLMS	granzyme 3 (EC 3.4
132	336.5	24.5	251	2	TL0262	u-plasminogen acti
133	336.5	24.5	251	2	PLC235	plasmin (EC 3.4.21
134	336.5	24.5	638	1	KQMSPL	maet cell serine p
135	336	24.5	496	1	KPBO	plasma kallikrein
136	336	24.5	790	1	PLPB	coagulation factor
137	335.5	24.4	258	4	S70439	plasmin (EC 3.4.21
138	333	24.2	245	1	KYBOA	pancreatic elastas
139	333	24.2	285	2	I48144	chymotrypsin (EC 3
140	332.5	24.2	638	1	KOKTPL	coagulation factor
141	332.5	24.2	810	2	I46260	plasma kallikrein
142	332.5	24.2	810	2	B30848	plasmin (EC 3.4.21
143	331.5	24.1	256	1	TRPF	plasmin (EC 3.4.21
144	331.5	24.1	275	2	S40007	trypsin-like prote
145	331	24.1	263	1	KYRMB	trypsin (EC 3.4.21
146	331	24.1	622	1	THBU	chymotrypsin (EC 3
147	330.5	24.1	247	1	KYHUCM	thrombin (EC 3.4.2
148	330.5	24.1	560	1	JC4795	chymase (EC 3.4.21
149	330	24.0	184621	2	I46421	plasma hyaluronan-
150	330	24.0	4548	1	S00657	coagulation factor
151	329.5	24.0	226	2	JR0151	apoptotrin(a) (EC
152	329.5	24.0	237	2	S68702	myronase (EC 3.4.-
153	329.5	24.0	269	2	C68823	trypase (EC 3.4.2
154	328.5	24.0	1420	2	A32869	pancreatic elastas
155	328.5	23.9	455	2	A61545	apolipoprotein(a)
156	328.5	23.9	455	2	A47547	plasmin (EC 3.4.21
157	328	23.9	452	1	A30351	serine proteinase
158	327.5	23.8	266	2	S54146	coagulation factor
159	327	23.8	244	2	S72219	trypsin (EC 3.4.21
160	327	23.8	259	2	S68424	chymotrypsin B - A
161	326.5	23.8	248	1	PRMSC2	allergen Der f III
162	326.5	23.8	266	1	BLPG	granzyme C (EC 3.4
163	326	23.7	248	2	S33755	pancreatic elastas
164	324	23.6	274	2	A45754	granzyme-like prote
165	324	23.6	459	2	J00419	trypase (EC 3.4.2
166	324	23.6	1019	1	A56318	coagulation factor
167	323.5	23.5	466	1	KFHU7	enteropeptidase (B
168	322	23.4	699	1	I54763	coagulation factor
169	321.5	23.4	251	2	JC2125	Ra-reactive factor
170	321	23.4	226	1	KCUF	chymase (EC 3.4.21
171	321	23.4	226	1	S69370	bradykinin (EC 3.4
172	321	23.4	247	2	S64708	chymase - bovine
173	321	23.4	248	2	A43520	duodenase (EC 3.4.21
174	321	23.4	269	2	B32410	natural killer cel
175	321	23.4	655	1	A46688	mastocytoma protei
						hepatocyte growth
176	320.5	23.3	247	1	PRMSCL	granzyme B (EC 3.4
177	319.5	23.3	559	1	A29941	t-plasminogen acti
178	319	23.2	1034	1	A53663	enteropeptidase (E
179	318.5	23.2	460	2	B61545	plasmin (EC 3.4.21
180	318	23.1	265	2	TL0495	chymotrypsin (EC 3
181	318	23.1	271	2	I46580	factor IX - pig (f
182	318	23.1	274	2	I47078	coagulation factor
183	318	23.1	618	2	A35827	thrombin (EC 3.4.2
184	317.5	23.1	245	1	KYBO	chymotrypsin (EC 3
185	317.5	23.1	245	2	A36692	cytotoxic T-lympho
186	317	23.0	246	1	A46504	granzyme M (EC 3.2
187	316.5	23.0	246	1	A46504	chymase (EC 3.4.21
188	315.5	23.0	254	1	BLRT1	trypsin-like prote
189	315.5	23.0	266	1	TRW3Y	pancreatic elastas
190	315.5	23.0	392	1	A30100	serine proteinase
191	315.5	23.0	492	1	EXBO	coagulation factor
192	315	22.9	248	2	S43259	granzyme-like prote
193	315	22.9	617	2	S10511	thrombin (EC 3.4.2
194	315	22.9	666	1	A59271	Ra-reactive factor
195	314	22.9	275	2	S40005	trypsin (EC 3.4.21
196	313	22.8	613	2	S15468	complement C3b/C4b
197	313	22.8	855	2	JC7731	membrane-bound arg
198	312.5	22.7	274	2	S40004	trypsin-related pr
199	312.5	22.7	615	1	KFHU2	coagulation factor
200	311.5	22.7	761	2	JCS759	brain-specific ser
201	311	22.6	261	2	S40162	cathepsin G (EC 3
202	311	22.6	431	1	S47538	acrosin (EC 3.4.21
203	311	22.6	433	1	JN0560	u-plasminogen acti
204	311	22.6	1035	1	A43090	enteropeptidase (B
205	310.5	22.6	247	1	PRRG	maet cell proteina
206	310.5	22.6	559	1	A35029	t-plasminogen acti
207	310	22.6	275	2	I46712	factor IX - rabbit
208	309.5	22.5	482	1	EXRT	coagulation factor
209	307	22.3	250	2	S55493	serine proteinase
210	307	22.3	259	1	S49129	chymotrypsin (EC 3
211	307	22.3	375	1	S00845	hepsin (EC 3.4.21.
212	306.5	22.3	417	1	A23689	limulus clotting e
213	305.5	22.2	236	2	I42696	thrombin (EC 3.4.2
214	305	22.2	281	1	A61021	granzyme B (EC 3.4
215	304	22.1	149	1	KQMSM	tissue kallikrein
216	304	22.1	268	2	C42696	thrombin (EC 3.4.2
217	304	22.1	236	2	S68825	pancreatic elastas
218	304	22.1	562	1	UKHUT	t-plasminogen acti
219	303.5	22.1	244	2	A46721	chymase (EC 3.4.21
220	303.5	22.1	309	2	B48878	coagulation factor
221	303	22.1	139	2	T08808	hypothetical prote
222	302.5	22.0	196	2	T08808	maet cell proteina
223	302.5	22.0	273	2	S40003	trypsin-related pr
224	302.5	22.0	1113	2	JR0315	oviductin (EC 3.4.
225	302.5	22.0	268	2	S68825	low-density lipopr
226	302	22.0	394	2	J50600	pancreatic elastas
227	302	22.0	477	1	A34369	t-plasminogen acti
228	302	22.0	477	1	J50598	t-plasminogen acti
229	302	22.0	255	2	A27122	cathepsin G (EC 3.
230	301	21.9	431	2	J50599	t-plasminogen acti
231	301	21.9	442	1	UKRG	u-plasminogen acti
232	300.5	21.9	245	2	A48598	kallikrein-like se
233	300	21.8	235	2	B42696	thrombin (EC 3.4.2
234	299.5	21.8	246	1	A48678	maet cell proteina
235	299.5	21.8	258	2	S44164	chymotrypsin (EC 3
236	299.5	21.8	436	2	JX0172	acrosin (EC 3.4.21
237	299.5	21.8	437	2	S18407	acrosin (EC 3.4.21
238	299	21.8	191	2	S54115	complement factor
239	298.5	21.7	249	1	A35842	chymase (EC 3.4.21
240	298.5	21.7	270	2	B29934	pancreatic elastas
241	298.5	21.7	407	1	KFH07	coagulation factor
242	297	21.6	237	1	TRCY1	trypsin (EC 3.4.21
243	297	21.6	260	2	S26043	chymase (EC 3.4.21
244	297	21.6	418	2	A37344	acrosin (EC 3.4.21
245	297	21.6	477	2	J50597	t-plasminogen acti
246	297	21.6	248	1	S01007	granzyme F (EC 3.4
247	296.5	21.6	248	1	T13596	trypsin homolog -
248	296	21.5	281	2		

249	295.5	21.5	239	2	G42696	thrombin (EC 3.4.2
250	295.5	21.5	433	1	UKMS	u-plasminogen acti
251	294	21.4	247	2	S23504	chymase (EC 3.4.21
252	294	21.4	303	2	T13598	trypsin homolog -
253	293.5	21.4	431	1	UKHU	u-plasminogen acti
254	293	21.3	234	2	F42696	thrombin (EC 3.4.2
255	293	21.3	247	2	S59135	maat cell proteina
256	293	21.3	247	2	A38894	seine proteinase
257	293	21.3	265	2	JS0260	seine proteinase
258	293	21.3	433	1	UKBA1	u-plasminogen acti
259	292.5	21.3	236	2	A28566	T-cell suppressor
260	291.5	21.2	216	1	KYVH20	chymotrypsin (EC 3
261	291	21.2	271	2	S41308	seine proteinase
262	289.5	21.1	248	2	A33412	cytotoxic T-lympho
263	289	21.0	583	2	A29154	complement factor
264	288.5	21.0	270	2	A29934	pancreatic elastas
265	288.5	21.0	1047	2	A55617	masquerade precurs
266	288	21.0	268	2	QJ1473	pancreatic elastas
267	288	21.0	421	2	S29599	acrosin (EC 3.4.21
268	287.5	20.9	235	2	H42696	thrombin (EC 3.4.2
269	287.5	20.9	603	2	S28941	coagulation factor
270	286.5	20.9	218	1	KYVH2C	chymotrypsin (EC 3
271	286	20.8	254	2	S35585	chymotrypsin-like
272	285.5	20.8	235	2	D42696	thrombin (EC 3.4.2
273	282.5	20.6	331	2	T27906	hypothetical prote
274	282	20.5	416	1	S33777	hepsin (EC 3.4.21
275	280	20.4	254	2	S65465	trypsin-like prote
276	278.5	20.3	593	2	S45281	coagulation factor
277	277.5	20.2	266	2	JC4850	trypsin-like prote
278	276	20.1	430	1	A24702	seine proteinase
279	276	20.1	488	1	EXHU	coagulation factor
280	275.5	20.1	240	1	CPBOA3	procarboxypeptidas
281	275	20.0	237	2	S55378	seine proteinase
282	274.5	20.0	695	1	S05008	complement subcomp
283	273	19.9	247	2	S45113	granzyme-like prot
284	273	19.9	265	2	T15451	hypothetical prote
285	272.5	19.8	432	1	S18932	u-plasminogen acti
286	272	19.8	475	1	EXCH	coagulation factor
287	272	19.8	688	1	CIHUS	complement subcomp
288	271	19.7	2616	2	A57096	ndel protein prec
289	270	19.7	694	2	JC6554	complement subcomp
290	269.5	19.6	248	2	S33756	granzyme-like prot
291	269	19.6	256	1	PRHU3	proteinase 3 (EC 3
292	268.5	19.5	420	2	A55283	acrosin (EC 3.4.21
293	265	19.3	415	1	A34170	acrosin (EC 3.4.21
294	264.5	19.3	256	2	T10109	trypsin (EC 3.4.21
295	264.5	19.3	264	2	S32794	trypsin-like prote
296	263.5	19.2	251	1	TRHU4Z	azurocidin precurs
297	261.5	19.0	366	2	JR0105	testicular seine
298	261.5	19.0	421	1	S11674	acrosin (EC 3.4.21
299	259	18.9	248	2	S01006	cytotoxic T-lympho
300	258.5	18.8	252	2	A36172	procytotoxic T-lym
301	258.5	18.8	285	2	T35195	probable seine pr
302	257.5	18.7	254	2	S49329	trypsin-like prote
303	256	18.6	403	2	C62228	probable trypsin V
304	252	18.3	400	1	A48050	coagulation factor
305	248	18.0	367	2	J50104	testicular factor
306	247	18.0	243	2	A56338	venom proteinase (
307	245	17.8	711	1	A47136	macrophage-stimula
308	244.5	17.8	716	1	A40332	macrophage-stimula
309	239.5	17.4	265	2	I48679	neutrophil elastas
310	237.5	17.3	232	2	S32398	seine proteinase
311	235.5	17.1	198	2	S06176	cytotoxic T-lympho
312	235.5	17.1	716	1	JC5061	macrophage-stimula
313	235	17.1	96	2	A05308	tissue kallikrein
314	235	17.1	230	2	A27802	hyaluronidase C (EC 3
315	234.5	17.1	219	1	TRGUAZ	azurocidin - pig
316	233	17.0	705	1	CIHURB	complement subcomp
317	231.5	16.8	230	2	I48685	maat cell proteina
318	227.5	16.6	230	2	JC4170	trypsin-like prote
319	227	16.5	259	1	TRSMG	trypsin (EC 3.4.21
320	226	16.4	728	1	JH0579	hepatocyte growth
321	225	16.4	548	2	D82175	probable trypsin V
322	220.5	16.0	267	1	ELHUL	leukocyte elastase
323	217.5	15.8	710	1	I51283	hepatocyte growth
324	216	15.7	728	1	A35644	hepatocyte growth
325	216	15.7	728	1	A60185	hepatocyte growth
326	204.5	14.9	177	2	S23505	chymase (EC 3.4.21
327	201	14.6	214	2	S17680	fibrinolytic prote
328	197.5	14.4	213	2	S17537	fibrinolytic prote
329	196	14.3	248	2	S49323	chymotrypsin (EC 3
330	192.5	14.0	763	2	I50807	complement factor
331	189.5	13.8	94	2	PC2013	tissue kallikrein
332	182	13.2	104	2	S15395	tissue kallikrein-
333	180	13.1	258	2	G02959	heptogloblin - rhes
334	179.5	13.1	149	2	S35208	seine proteinase
335	178	13.0	347	1	HPHUR	heptogloblin precu
336	177	12.9	347	1	HPHU1	heptogloblin precu
337	177	12.9	406	1	HPHU2	heptogloblin precu
338	176.5	12.8	760	1	C2MS	classical-compleme
339	176	12.8	735	2	T35778	probable fusidic a
340	174.5	12.7	377	2	C88710	protein C43g2.5 (I
341	174	12.7	161	2	I48158	coagulation factor
342	174	12.7	330	2	B82415	probable seine pr
343	172	12.5	346	2	I36942	heptogloblin - chim
344	171	12.4	159	2	S35202	proteinase 2 - buf
345	171	12.4	258	2	I36945	heptogloblin Hp - c
346	171	12.4	345	2	I36941	heptogloblin - chim
347	170	12.4	347	2	G00006	heptogloblin - biac
348	169	12.3	329	1	HPDG	heptogloblin precu
349	168	12.2	66	2	I52972	kallikrein - mouse
350	168	12.2	154	2	S35207	proteinase 7 - buf
351	166	12.1	258	2	I36947	heptogloblin Hpp -
352	166	12.1	349	2	I36944	heptogloblin - chim
353	166	12.1	752	1	C2HU	complement C2 prec
354	165	12.0	161	2	I62744	coagulation factor
355	165	12.0	347	1	HPMS	heptogloblin precu
356	159.5	11.6	152	2	S35209	seine proteinase
357	159	11.6	126	2	A23473	chymotrypsin-like
358	158.5	11.5	264	2	A28942	pancreatic elastas
359	157.5	11.5	764	1	BBHU	complement factor
360	154.5	11.2	747	2	I51579	complement factor
361	153.5	11.2	761	1	BBMS	complement factor
362	152.5	11.1	159	2	I84615	coagulation factor
363	152	11.1	181	2	T08805	hypothetical prote
364	151.5	11.0	152	2	S35203	seine proteinase
365	148	10.8	81	2	A18966	tissue kallikrein
366	145.5	10.6	82	2	T46510	hypothetical prote
367	138.5	10.1	158	2	S35201	seine proteinase
368	138	10.0	153	2	S35204	proteinase 4 - buf
369	137	10.0	743	2	T34853	probable fusidic a
370	136.5	9.9	152	2	S35206	seine proteinase
371	135.5	9.9	46	2	I49416	glangular kallikre
372	132	9.6	347	1	HPRT	heptogloblin precu
373	129.5	9.4	396	1	KXBOZ	plasma protein 2 -
374	127.5	9.3	69	2	S28195	tissue kallikrein
375	127.5	9.3	72	2	S28196	tissue kallikrein
376	126	9.2	80	2	A05324	gamma-remn (EC 3.
377	123.5	9.0	137	2	S55364	seine proteinase
378	123.5	9.0	151	2	S35205	proteinase 5 - buf
379	122.5	8.9	75	2	A37002	carboxobin 1 (EC 3
380	115.5	8.4	422	1	KXHUZ	plasma protein 2 p
381	114.5	8.3	61	2	S44461	elastase (EC 3.4.2
382	109.5	8.0	85	2	P50049	seine proteinase
383	108	7.9	333	2	T15257	hypothetical prote
384	104.5	7.6	256	2	A5653	trypsin-related, pr
385	104	7.6	49	2	B24636	tissue kallikrein
386	103.5	7.5	64	2	T34423	prostetic arginine
387	99.5	7.2	340	2	S34672	hypothetical prote
388	97	7.1	388	2	AH2387	alkaline seine pr
389	96.5	7.0	416	2	G71965	glycine hydroxymet
390	94.5	6.9	416	2	S44462	elastase (EC 3.4.2
391	93.5	6.8	773	2	PRSMG	streptogristin B (E
392	93.5	6.8	299	1	G64542	glycine hydroxymet
393	92.5	6.7	416	2	A18671	tissue kallikrein
394	91	6.6	31	2		

395	90.5	6.6	48	2	A61331	468	78	5.7	4006	2	T09070	probable tenascin
396	90	6.6	1745	1	S19694	469	77.5	5.6	438	2	S53797	collagen alpha cha
397	90	6.6	2825	2	T14271	470	77.5	5.6	921	2	S42617	collagen alpha 1(I)
398	89	6.5	4557	2	A53669	471	77.5	5.6	1669	1	CGMS4B	collagen alpha 1(I)
399	89	6.5	1737	2	T00209	472	77.5	5.6	1691	1	CGH56B	collagen alpha 6(I)
400	88.5	6.4	2205	1	MMWVRN	473	77.5	5.6	2907	2	A57278	fibritillin-2 precur
401	88.5	6.4	3002	2	A47221	474	77	5.6	517	2	T47134	hypothetical prote
402	87.5	6.4	278	2	AH0282	475	77	5.6	553	2	F75407	probable transport
403	87.5	6.4	1582	2	T15308	476	77	5.6	668	2	A41234	melanocyte-specific
404	86.5	6.3	34	2	I49417	477	77	5.6	710	2	T31502	hypothetical prote
405	86.5	6.3	38	2	I70029	478	77	5.6	1104	2	T38869	transcription fact
406	86.5	6.3	38	2	I70036	479	77	5.6	3566	1	A40701	tenascin-X precurs
407	86.5	6.3	38	2	I70036	480	77	5.6	315	2	A44984	collagen - nematod
408	86	6.3	502	2	A46784	481	76.5	5.6	295	2	H83096	probable pyrophosp
409	86	6.3	2704	2	S09118	482	76.5	5.6	348	2	A34705	collagen - Caenorh
410	86	6.2	398	2	B75254	483	76.5	5.6	382	2	PC2053	alkaline proteinas
411	85	6.2	411	2	T34585	484	76.5	5.6	469	1	S29126	propeptidin precurs
412	85	6.2	2718	2	A23475	485	76.5	5.6	1042	1	CGCH1S	collagen alpha 1(I)
413	85	6.2	1023	2	T30257	486	76.5	5.6	1453	2	S21626	collagen alpha 1(I)
414	84.5	6.1	1023	2	T2637	487	76.5	5.6	257	2	T52298	collagen alpha 1(X)
415	84.5	6.1	2871	2	A55567	488	76	5.5	301	2	C84474	squamosa promoter
416	84.5	6.1	133	2	T17300	489	76	5.5	361	2	S30325	hypothetical prote
417	84	6.1	273	2	B85765	490	76	5.5	455	2	AP2949	hypothetical prote
418	84	6.1	305	2	S44767	491	76	5.5	455	2	AP2949	ornithine decarbox
419	84	6.1	458	2	T36442	492	76	5.5	512	2	B98333	probable ornithine
420	83.5	6.1	725	2	B96596	493	76	5.5	608	2	T05442	glycine-rich prote
421	83.5	6.1	133	2	T17300	494	76	5.5	677	2	S23296	collagen alpha 2(I)
422	83.5	6.1	788	2	A37057	495	76	5.5	920	2	B34493	collagen alpha 1(I)
423	83.5	6.1	1433	2	A46053	496	76	5.5	986	1	OYURGA	spesate receptor P
424	83	6.0	266	2	T21597	497	76	5.5	396	2	A42551	genome polyprotein
425	83	6.0	273	2	H64915	498	76	5.5	481	2	T26950	interleukin-3 rece
426	82.5	6.0	522	2	T29767	499	75.5	5.5	596	2	A35628	hypothetical prote
427	82.5	6.0	644	2	C75457	500	75.5	5.5	621	2	T50024	amyloid precursor-
428	82.5	6.0	436	2	AH2515	501	75.5	5.5	653	2	A46362	hypothetical prote
429	82	6.0	90	2	JE0210	502	75.5	5.5	677	2	T37310	collagen alpha 2(I)
430	82	6.0	357	2	T21152	503	75.5	5.5	688	2	A53330	collagen alpha 1(X)
431	82	6.0	418	2	A46076	504	75.5	5.5	697	2	T18681	hypothetical prote
432	82	6.0	418	2	A60341	505	75.5	5.5	1142	2	TX0369	collagen alpha 2(I)
433	81.5	5.9	244	2	UC4708	506	75.5	5.5	291	2	T20083	hypothetical prote
434	81.5	5.9	323	2	T27450	507	75	5.5	391	2	T26576	hypothetical prote
435	81.5	5.9	779	1	CGBO1S	508	75	5.5	437	2	I50696	collagen alpha 1(I)
436	81.5	5.9	2229	2	T16199	509	75	5.5	809	1	IJBODC	properdin - mouse
437	81	5.9	247	2	T26688	510	75	5.5	864	1	EAR7	desmocollin 2b pre
438	81	5.9	428	2	T24769	511	75	5.5	902	2	T26775	desmocollin 2a pre
439	80.5	5.9	283	2	T29837	512	75	5.5	1140	2	AE0180	elastin precursor
440	80.5	5.9	290	2	T46470	513	75	5.5	1236	1	VMWME	hypothetical prote
441	80.5	5.9	294	2	T29839	514	75	5.5	1514	2	A45407	structural polypro
442	80.5	5.9	1464	1	CGHUS	515	75	5.5	1752	2	A45407	multi resistance p
443	80.5	5.9	812	2	S31521	516	75	5.5	177	2	AB3269	collagen alpha 3(I)
444	80.5	5.9	2871	2	A55624	517	75	5.5	246	2	S30144	outer membrane lip
445	80	5.8	248	2	A48853	518	75	5.5	601	2	G70963	osmotic-like prote
446	80	5.8	333	2	T23668	519	74.5	5.4	638	1	A31845	probable glycosyl
447	80	5.8	550	2	B50723	520	74.5	5.4	791	2	A31246	nitrous-oxide redu
448	79.5	5.8	550	2	B85574	521	74.5	5.4	832	2	A31246	probable iron-regu
449	79.5	5.8	550	2	T20435	522	74.5	5.4	880	2	S00670	neurogenic protein
450	79	5.7	295	2	T19220	523	74.5	5.4	931	2	S13580	gene Delta protein
451	79	5.7	295	2	T20436	524	74.5	5.4	1496	1	CGH02V	neurogenic repetit
452	79	5.7	782	2	A61625	525	74.5	5.4	1630	1	CGHUIB	collagen alpha 1(I)
453	79	5.7	921	2	S60495	526	74.5	5.4	1763	2	S16366	collagen alpha 2(I)
454	79	5.7	1758	2	T29350	527	74.5	5.4	246	2	S29328	collagen alpha 4(I)
455	79	5.7	1758	2	T29350	528	74.5	5.4	246	2	LMRPS	complement subcomp
456	78.5	5.7	1758	2	T29350	529	74.5	5.4	273	2	AE0682	pulmonary surfacta
457	78.5	5.7	310	2	T22641	530	74.5	5.4	302	2	A31921	probable secreted
458	78.5	5.7	504	2	T34995	531	74	5.4	325	2	T18594	collagen dpy-13 pr
459	78.5	5.7	1315	2	A56101	532	74	5.4	457	2	T04226	hypothetical prote
460	78.5	5.7	2115	2	B56101	533	74	5.4	470	2	D41977	retinoid receptor
461	78.5	5.7	2214	2	S38480	534	74	5.4	513	2	S11439	cellulose 1,4-beta
462	78.5	5.7	2214	2	S38480	535	74	5.4	566	2	S69887	hemagglutinin prec
463	78.5	5.7	4135	2	T16305	536	74	5.4	614	2	T33149	hypothetical prote
464	78.5	5.7	4545	1	S25111	537	74	5.4				
465	78	5.7	300	2	T36768	538	74	5.4				
466	78	5.7	359	2	B83112	539	74	5.4				
467	78	5.7	394	2	T33641	540	74	5.4				

541	74	5.4	886	2	150694	collagen alpha 1(I
542	74	5.4	1124	1	158388	protein-tyrosine k
543	74	5.4	1413	1	T26457	hypothetical prote
544	74	5.4	1670	1	CGHUB	collagen alpha 3(I
545	74	5.4	1677	2	T14267	Xin protein, stage
546	73.5	5.3	246	2	T16403	hypothetical prote
547	73.5	5.3	294	2	T29838	hypothetical prote
548	73.5	5.3	305	2	B84413	hypothetical prote
549	73.5	5.3	321	2	T28760	hypothetical prote
550	73.5	5.3	346	2	UA0159	cysteine proteinas
551	73.5	5.3	411	2	A65184	arylsulfatase acti
552	73.5	5.3	482	2	AE0839	succinate-semialde
553	73.5	5.3	483	2	D83613	succinate-semialde
554	73.5	5.3	525	1	CGHUB	cellulose 1,4-beta
555	73.5	5.3	680	1	CGHUB	collagen alpha 1(X
556	73.5	5.3	724	1	A48569	antigen Em100 - E1
557	73.5	5.3	791	2	D64629	liron-regulated out
558	73.5	5.3	1806	1	CGHUB	collagen alpha 1(X
559	73	5.3	50	2	S55674	cerastocytin (EC 3
560	73	5.3	295	2	T22833	hypothetical prote
561	73	5.3	360	2	T36763	probable secreted
562	73	5.3	508	2	B70865	probable transmemb
563	73	5.3	597	2	S71352	metalloproteinase
564	73	5.3	662	2	I18400	melanoma-associate
565	73	5.3	707	1	TSBYAB	tryptophan synthas
566	73	5.3	768	2	SA3768	transcription acti
567	73	5.3	767	2	T05662	hypothetical prote
568	73	5.3	881	2	S25445	nitrate reductase
569	73	5.3	997	2	A60776	230k bullous pemph
570	73	5.3	1339	2	JC4387	epidermal growth f
571	73	5.3	1744	1	SA0991	collagen alpha 1(I
572	73	5.3	2207	1	GNNV5P	genome polypotein
573	73	5.3	2555	2	A40043	notch protein homo
574	73	5.3	3061	1	JN0545	genome polypotein
575	73	5.3	3623	2	T08618	intrinsic factor-B
576	72.5	5.3	155	1	TIZM1	trypsin/factor XII
577	72.5	5.3	230	2	D85553	probable chaperone
578	72.5	5.3	230	2	A90703	probable chaperone
579	72.5	5.3	230	2	B64785	molecular chaperon
580	72.5	5.3	286	2	C81681	dihydrodipicolinat
581	72.5	5.3	302	2	T32872	hypothetical prote
582	72.5	5.3	328	2	JC5350	2-nitrotoluene red
583	72.5	5.3	362	2	T35287	probable secreted
584	72.5	5.3	488	2	T47697	Regulator of chrom
585	72.5	5.3	606	2	T08180	Pf20 protein, micr
586	72.5	5.3	1132	2	T03844	telomerase catalyt
587	72.5	5.3	1497	2	I49607	pirocollagen type V
588	72.5	5.3	1514	2	T34869	glutamate synthase
589	72.5	5.3	207	2	T46415	hypothetical prote
590	72	5.2	220	2	T18553	probable O-methylt
591	72	5.2	229	2	D95398	hypothetical prote
592	72	5.2	258	2	A29259	Ubx protein - Fru1
593	72	5.2	372	2	A56123	streptogristin D (E
594	72	5.2	597	2	B37057	integrin beta-6 ch
595	72	5.2	673	2	F89101	protein F25E5.7 [i
596	72	5.2	691	2	T44543	probable bacteriop
597	72	5.2	814	2	T49207	receptor kinase-11
598	72	5.2	957	2	T15976	hypothetical prote
599	72	5.2	1220	2	A56136	jaeged protein pre
600	72	5.2	2150	1	GNNVH2	genome polypotein
601	72	5.2	2194	1	GNNVE7	genome polypotein
602	72	5.2	2205	1	GNNV2W	genome polypotein
603	71.5	5.2	38	2	A45526	collagen homolog A
604	71.5	5.2	236	2	T24799	hypothetical prote
605	71.5	5.2	283	2	JC5579	chymotrypsin-like
606	71.5	5.2	284	2	G70732	probable thiosulfa
607	71.5	5.2	297	2	T18966	hypothetical prote
608	71.5	5.2	305	2	T20906	hypothetical prote
609	71.5	5.2	466	2	I19707	probable indoleace
610	71.5	5.2	524	2	T04623	criciteirin F2009.2
611	71.5	5.2	547	2	T29717	hypothetical prote
612	71.5	5.2	665	1	VCNVKA	env polypotein pr
613	71.5	5.2	793	2	AH2126	hypothetical prote
614	71.5	5.2	895	2	T49010	hypothetical prote
615	71.5	5.2	918	2	JC4361	scavenger receptor
616	71	5.2	181	2	S56532	hypothetical 20k p
617	71	5.2	316	2	S25264	virk protein - Shi
618	71	5.2	369	2	E70606	probable regulator
619	71	5.2	407	2	A10595	imidazolonepropion
620	71	5.2	458	2	T31631	hypothetical prote
621	71	5.2	490	2	T37884	transcription fact
622	71	5.2	497	2	B42827	interleukin enhanc
623	71	5.2	575	2	A97635	adenine deaminase
624	71	5.2	575	2	AC2858	adenine deaminase
625	71	5.2	639	2	D70931	hypothetical glyci
626	71	5.2	818	2	B75606	hypothetical prote
627	71	5.2	883	2	T51231	hypothetical prote
628	71	5.2	1230	2	B64654	outer membrane pro
629	71	5.2	1391	2	T20406	hypothetical prote
630	71	5.2	1691	1	S22917	collagen alpha 5(I
631	71	5.2	1717	1	A45558	epidermal growth f
632	71	5.2	2164	1	GNNV89	genome polypotein
633	71	5.2	2531	2	S18188	notch protein homo
634	71	5.2	2531	2	T16743	hypothetical prote
635	71	5.2	3512	2	T17121	CPT protein - midg
636	70.5	5.1	238	2	S28001	osmotin-like prote
637	70.5	5.1	284	2	T29528	hypothetical prote
638	70.5	5.1	290	2	A81176	fructokinase homo
639	70.5	5.1	325	2	T06784	GTP-binding protei
640	70.5	5.1	325	2	T09613	probable GTP-bindi
641	70.5	5.1	339	2	T22607	hypothetical prote
642	70.5	5.1	356	2	S66348	cysteine proteinas
643	70.5	5.1	366	2	S11449	collagen short cha
644	70.5	5.1	396	1	TRYXB4	alpha-lytic protei
645	70.5	5.1	400	2	T35106	probable secreted
646	70.5	5.1	423	2	A41297	collagen 13, nonfi
647	70.5	5.1	585	2	T37526	probable transcrip
648	70.5	5.1	627	2	T35608	polyketide hydroxy
649	70.5	5.1	630	2	T43460	hypothetical prote
650	70.5	5.1	860	1	EMMS	elastin precursor
651	70.5	5.1	920	2	A45748	collagen alpha 1(V
652	70.5	5.1	1342	2	A36223	kinase-related tra
653	70.5	5.1	1414	1	S23809	collagen alpha 2(I
654	70.5	5.1	1486	1	B40333	collagen alpha 1(I
655	70.5	5.1	1747	2	A54121	collagen alpha-4 c
656	70.5	5.1	3198	2	A43426	collagen alpha 2 f
657	70	5.1	261	2	SA40210	chlorophyll a/b-bi
658	70	5.1	283	2	JB0170	collagen col-19 -
659	70	5.1	285	2	S60598	collagen alpha cha
660	70	5.1	300	2	T11929	hypothetical prote
661	70	5.1	304	2	T26185	hypothetical prote
662	70	5.1	304	2	T26184	hypothetical prote
663	70	5.1	313	2	T26465	hypothetical prote
664	70	5.1	315	2	C95941	probable transcrip
665	70	5.1	343	2	UQ2370	hemagglutinin - in
666	70	5.1	389	2	I49263	potential oncogene
667	70	5.1	389	2	A59392	Wnt10b protein pre
668	70	5.1	395	1	T45547	arylsulfatase acti
669	70	5.1	402	2	H82228	indazolonepropion
670	70	5.1	485	2	F97228	glu-tRNAcin amidot
671	70	5.1	548	2	H82432	eucrose-6-phospat
672	70	5.1	560	2	D84205	hypothetical prote
673	70	5.1	561	2	C75543	6-aminohehexanoate-c
674	70	5.1	671	1	CGRT1S	collagen alpha 1(I
675	70	5.1	798	2	S23297	collagen alpha 1(X
676	70	5.1	798	2	T28996	hypothetical prote
677	70	5.1	863	2	A53034	gag polypotein -
678	70	5.1	877	2	S49197	envelope protein p
679	70	5.1	938	2	D84480	hypothetical prote
680	70	5.1	1188	2	D86236	protein F14N23.5 [
681	70	5.1	1366	2	T35985	probable large pro
682	70	5.1	2043	2	T18524	beavenger receptor
683	70	5.1	2206	1	GNNV4P	genome polypotein
684	70	5.1	2206	1	GNNV27	genome polypotein
685	70	5.1	2206	2	S03832	genome polypotein
686	70	5.1	4391	2	A38096	perlecan precursor

687	69.5	5.1	126	2	S47010	Ig heavy chain V4.	760	68.5	5.0	337	2	H86582	CTF 368 hypocheica
688	69.5	5.1	184	2	E82345	probable galactosy	761	68.5	5.0	357	2	H89819	conserved hypothe
689	69.5	5.1	244	1	LNMSMC	mannose-binding le	762	68.5	5.0	372	2	S60207	femf protein - Str
690	69.5	5.1	248	1	LNMSPS	pulmonary surfacta	763	68.5	5.0	412	2	G86003	probable transport
691	69.5	5.1	250	2	S30157	osmotic precursor	764	68.5	5.0	412	2	A91158	probable transport
692	69.5	5.1	275	2	A84179	endoenzyme IV [i	765	68.5	5.0	412	2	B65134	protein transport
693	69.5	5.1	303	2	T19289	hypotheical prote	766	68.5	5.0	427	2	S57776	cyteine proteinas
694	69.5	5.1	337	2	T23794	hemagglutinin - in	767	68.5	5.0	487	2	AF2692	MFS permease [impo
695	69.5	5.1	353	2	S15785	collagen alpha 1(I)	768	68.5	5.0	528	2	B33485	hypotheical prote
696	69.5	5.1	356	2	S15907	collagen alpha 3(V	769	68.5	5.0	537	2	B33485	spore coat protein
697	69.5	5.1	382	2	S20375	ABC transporter (p	770	68.5	5.0	544	2	G87330	conserved hypothe
698	69.5	5.1	432	2	P96919	cysteine proteinas	771	68.5	5.0	547	2	A36046	collagen alpha cha
699	69.5	5.1	466	2	T06416	hypotheical prote	772	68.5	5.0	575	2	UC7727	4-alpha-D-(1->4) -
700	69.5	5.1	482	2	S76475	NH3-dependent NAD	773	68.5	5.0	579	2	B45266	MP-L-K protein prec
701	69.5	5.1	545	2	C82617	integrin beta-5 ch	774	68.5	5.0	634	1	S24384	nitrous-oxide redu
702	69.5	5.1	656	2	UC2005	phosphorylform	775	68.5	5.0	635	2	A45266	MP-L-P protein prec
703	69.5	5.1	739	2	C87559	trophinin - human	776	68.5	5.0	673	1	CG806C	collagen alpha 1(I
704	69.5	5.1	749	2	I38488	collagen alpha 1(X	777	68.5	5.0	674	2	S13301	collagen alpha 1(X
705	69.5	5.1	1024	2	S18251	DNA-directed DNA p	778	68.5	5.0	677	2	P95910	probable membrane-
706	69.5	5.1	1181	2	C97851	collagen alpha 1(I	779	68.5	5.0	744	1	A34246	collagen alpha 1(V
707	69.5	5.1	1418	2	T45467	collagen alpha 1(I	780	68.5	5.0	744	1	S23298	collagen alpha 1(V
708	69.5	5.1	1464	2	S59856	collagen alpha 1(I	781	68.5	5.0	744	2	S15435	collagen alpha 1(V
709	69.5	5.1	1487	1	CGH06C	collagen alpha 1(X	782	68.5	5.0	888	2	S28791	collagen alpha 1(X
710	69.5	5.1	1603	2	S23810	probable polykeid	783	68.5	5.0	915	2	T21772	hypotheical prote
711	69.5	5.1	1986	2	S28353	tenascin precursor	784	68.5	5.0	927	2	T21772	hypotheical prote
712	69.5	5.1	2019	1	JQ1322	tenascin C - human	785	68.5	5.0	937	2	I53282	gene PACB4 protein
713	69.5	5.1	2201	2	A32160	pseudo-Kallikrein	786	68.5	5.0	1049	1	CG807S	collagen alpha 1(I
714	69	5.0	38	2	T01677	finger protein (cl	787	68.5	5.0	1419	2	A41182	collagen alpha 1(I
715	69	5.0	224	2	S06545	mannose-binding le	788	68.5	5.0	1487	2	B41182	collagen alpha 1(I
716	69	5.0	239	1	LNMSMA	hypotheical prote	789	68.5	5.0	2206	1	GNNY21	genome polyprotein
717	69	5.0	290	2	T24586	hypotheical prote	790	68.5	5.0	2403	2	A59386	sanko - human
718	69	5.0	290	2	T24590	streptogristin A (E	791	68.5	5.0	2482	2	I48922	cation-independent
719	69	5.0	294	2	T21668	guanine nucleotide	792	68.5	5.0	2483	1	A49617	insulin-like growt
720	69	5.0	297	1	PRSMAG	molybdome C-type	793	68.5	5.0	2560	1	I40457	peptide synthetase
721	69	5.0	327	2	B81829	cytochrome C-type	794	68.5	5.0	2715	2	T13049	eyelid - fruit fly
722	69	5.0	329	2	B81162	hypotheical prote	795	68.5	5.0	3106	1	S53868	laminin alpha-2 ch
723	69	5.0	334	1	S74957	hypotheical prote	796	68.5	5.0	4544	1	S02392	alpha-2-macroglobu
724	69	5.0	395	2	B41035	acetylaminidase - Myco	797	68.5	5.0	4660	2	T42737	gp330 protein prec
725	69	5.0	399	2	H84717	beta transducin -	798	68	4.9	175	1	A60010	early B1A 20K prot
726	69	5.0	406	2	A47696	hypotheical prote	799	68	4.9	177	2	S37749	collagen alpha 2(X
727	69	5.0	435	2	T39719	hydrotheical prote	800	68	4.9	229	1	S54799	nitrile hydratase
728	69	5.0	438	2	T50991	hydrotheical prote	801	68	4.9	237	2	A88640	protein C34H4.4 [l
729	69	5.0	441	2	A45565	cyteine proteinas	802	68	4.9	248	1	LNHUMC	mannose-binding le
730	69	5.0	469	2	A24450	collagen alpha 2(V	803	68	4.9	272	2	H87075	probable conserved
731	69	5.0	523	2	B95922	hypotheical ncle	804	68	4.9	289	2	T27708	hypotheical prote
732	69	5.0	532	2	P70580	hydrotheical glyci	805	68	4.9	297	2	T46864	nicotinate-nucleot
733	69	5.0	567	1	C55516	hydrogenase (Bc 1.	806	68	4.9	330	2	T26004	hypotheical prote
734	69	5.0	567	2	G85958	probable large sub	807	68	4.9	343	1	HMIWTA	hemagglutinin HAI
735	69	5.0	567	2	G91113	NMDH2 dehydrogenas	808	68	4.9	349	2	D72175	G2R protein - vari
736	69	5.0	613	2	T11464	collagen alpha 2(V	809	68	4.9	354	2	A35788	hemagglutinin - in
737	69	5.0	635	2	A57131	probable Tail-1-like	810	68	4.9	358	2	T26281	hypotheical prote
738	69	5.0	682	2	D84579	URB51 protein - sm	811	68	4.9	384	2	S46110	Wotch A protein -
739	69	5.0	950	2	S27473	collagen alpha 2(I	812	68	4.9	387	2	B49175	Gal beta-1, 3GalNA
740	69	5.0	1366	1	CGH0US	collagen alpha 1(I	813	68	4.9	404	2	A54871	glutamate dehydrog
741	69	5.0	1669	1	CGH0UB	hypotheical prote	814	68	4.9	412	2	FC6317	conjugat transfer
742	69	5.0	1749	2	S75071	laminin beta-1 cha	815	68	4.9	447	2	F82862	beta tubulin 1 - r
743	69	5.0	1786	1	MMHUB1	genome polyprotein	816	68	4.9	453	2	S49168	phosphotransferase
744	69	5.0	2207	1	S09553	protein-tyrosine-p	817	68	4.9	460	2	A39938	succinate-semialde
745	69	5.0	2209	1	GNNY2P	ALR protein - huma	818	68	4.9	484	2	P98208	aldehyde dehydroge
746	69	5.0	2450	1	S71625	ferredoxin - huma	819	68	4.9	484	2	AC3076	succinate-semialde
747	69	5.0	4957	2	T03455	vasotocin 2 / neur	820	68	4.9	543	2	A41285	hemagglutinin prec
748	69	5.0	5267	2	T03454	osmotic-like prote	821	68	4.9	566	1	HMTV	hemagglutinin prec
749	69	5.0	1272	2	F82617	collagen alpha 1(V	822	68	4.9	605	2	T15291	epitope-like protein
750	68.5	5.0	155	2	B31829	fructokinases homo	823	68	4.9	631	2	UC2345	Rhs element associ
751	68.5	5.0	233	2	S31829	hypotheical prote	824	68	4.9	656	2	G85731	collagen alpha 1(X
752	68.5	5.0	250	2	S25114	probable aryl alco	825	68	4.9	724	2	T27858	probable peroxidase
753	68.5	5.0	252	2	A55047	conserved hypothe	826	68	4.9	726	2	T35865	collagen alpha 5(I
754	68.5	5.0	285	2	T18814		827	68	4.9	743	1	S23779	
755	68.5	5.0	290	2	A11533		828	68	4.9	754	1	A55267	
756	68.5	5.0	323	2	T19142		829	68	4.9	756	2	S67433	
757	68.5	5.0	339	2	T32783		830	68	4.9				
758	68.5	5.0	336	1	S76928		831	68	4.9				
759	68.5	5.0	337	2	A72042		832	68	4.9				

833	68	4.9	759	2	B70585	hypothetical prote	906	67	4.9	651	2	A26581	beta-glucuronidase
834	68	4.9	864	2	A48266	protein-tyrosine k	907	67	4.9	653	2	G96675	hypothetical prote
835	68	4.9	972	2	A30363	glycoprotein GP330	908	67	4.9	686	2	JC7569	Delta-4 protein -
836	68	4.9	1223	2	T17345	hypothetical prote	909	67	4.9	737	2	S65758	nitrate reductase
837	68	4.9	1331	2	S05011	calcium channel al	910	67	4.9	756	2	AH1022	arginine decarboxy
838	68	4.9	1400	2	E90886	RNase core protein	911	67	4.9	884	2	T18649	hypothetical prote
839	68	4.9	1493	2	A44224	DNA repair helicase	912	67	4.9	919	2	T16150	hypothetical prote
840	68	4.9	1786	1	MMMS81	laminin beta-1 cha	913	67	4.9	1012	2	T13603	probable N-methyl-
841	68	4.9	2100	2	T03223	probable polyketid	914	67	4.9	1027	2	S28874	collagen alpha cha
842	68	4.9	2209	1	GNNY3P	genome polypotein	915	67	4.9	1034	2	JC5598	mucin - rat
843	68	4.9	2767	1	U1HU	thryoglobulin prec	916	67	4.9	1051	2	A35763	fibropellin Ia - s
844	67.5	4.9	73	1	HPRB	haaptoglobin precu	917	67	4.9	1064	2	A40136	DNA-binding protei
845	67.5	4.9	242	1	AG1868	hypothetical prote	918	67	4.9	1196	1	DNBEHF	major DNA-binding
846	67.5	4.9	247	1	LNRRBS	hypothetical prote	919	67	4.9	1196	1	DNBEV1	collagen alpha 2(I
847	67.5	4.9	286	2	S34665	collagen, cuticula	920	67	4.9	1373	1	A43291	collagen alpha 1(I
848	67.5	4.9	296	2	T21070	hypothetical prote	921	67	4.9	1466	1	CGH07L	collagen alpha 1(I
849	67.5	4.9	307	2	T16842	hypothetical prote	922	67	4.9	1632	2	C70752	probable ctcp1 prot
850	67.5	4.9	315	2	T34932	hypothetical prote	923	67	4.9	1705	2	S51672	adenylate cyclase
851	67.5	4.9	325	2	AE2384	hypothetical prote	924	67	4.9	1747	2	A45974	collagen type IV a
852	67.5	4.9	335	2	S02170	collagen alpha 1(I	925	67	4.9	1761	2	T13990	collagen type IV a
853	67.5	4.9	330	2	S46657	collagen alpha 1(X	926	67	4.9	1775	2	S31893	collagen alpha 1(I
854	67.5	4.9	337	2	A83026	hypothetical prote	927	67	4.9	1857	2	S31212	collagen alpha 1(X
855	67.5	4.9	339	2	E82211	conserved hypochet	928	67	4.9	1888	2	S78476	collagen alpha 1(X
856	67.5	4.9	356	2	A25918	thrombomodulin - b	929	67	4.9	2269	1	JQ1750	genome polypotein
857	67.5	4.9	369	2	T02150	probable (S)-2-hyd	930	67	4.9	2524	2	A35844	Xotch protein - Af
858	67.5	4.9	393	2	T31771	hypothetical prote	931	67	4.9	3282	2	E82750	hemagglutinin-like
859	67.5	4.9	399	2	C95943	probable choline u	932	66.5	4.8	35	2	I49403	complement factor
860	67.5	4.9	412	2	AB1000	type II secretion	933	66.5	4.8	119	2	S41111	pancreatic ribonuc
861	67.5	4.9	451	2	S65162	hypothetical prote	934	66.5	4.8	122	2	UL0047	Ig heavy chain V x
862	67.5	4.9	458	2	T10622	hypothetical prote	935	66.5	4.8	140	2	A49045	lg heavy chain V x
863	67.5	4.9	627	2	A70888	hypothetical prote	936	66.5	4.8	140	2	T21857	hypothetical prote
864	67.5	4.9	665	1	VCMVVR	env polypotein pr	937	66.5	4.8	243	2	S34794	osmocin - common t
865	67.5	4.9	674	2	T19268	hypothetical prote	938	66.5	4.8	244	1	LNRMTC	mannose-binding le
866	67.5	4.9	771	2	S35681	ESG protein - mous	939	66.5	4.8	251	2	G75495	hypothetical prote
867	67.5	4.9	846	1	PNECA	penicillin amidase	940	66.5	4.8	278	2	H87663	hypothetical prote
868	67.5	4.9	850	2	S56015	gastric mucin MUC5	941	66.5	4.8	294	2	G72706	hypothetical prote
869	67.5	4.9	861	2	A48825	Notch homolog Muc5	942	66.5	4.8	301	2	T23441	hypothetical prote
870	67.5	4.9	977	2	I52657	seizure-related pr	943	66.5	4.8	303	2	E90444	conserved hypochet
871	67.5	4.9	1010	2	T36383	probable large ATP	944	66.5	4.8	304	2	T22482	hypothetical prote
872	67.5	4.9	1091	1	PL0009	complement C3d/Eps	945	66.5	4.8	316	2	T19291	hypothetical prote
873	67.5	4.9	1208	2	T27832	hypothetical prote	946	66.5	4.8	337	2	S55932	NCA3 protein precu
874	67.5	4.9	1242	1	JDJBEC1	DNA-directed DNA p	947	66.5	4.8	345	2	AH0350	probable DNA-bindi
875	67.5	4.9	1373	2	J80095	gastric mucin MUC5	948	66.5	4.8	377	2	JC7535	chitinase (EC 3.2.
876	67.5	4.9	1574	2	T13954	MGP6 protein - ra	949	66.5	4.8	388	2	JC6164	clitumsporoxite p
877	67.5	4.9	1706	1	OYBRC	cytolysin - Borde	950	66.5	4.8	417	2	T08724	hypothetical prote
878	67.5	4.9	1810	1	A32230	tenascin precursor	951	66.5	4.8	428	2	T19309	hypothetical prote
879	67.5	4.9	1838	1	CGHUVI	collagen alpha 1(V	952	66.5	4.8	506	2	F83547	sodium/proline sym
880	67.5	4.9	1843	2	S18803	collagen alpha 1(V	953	66.5	4.8	560	2	H70466	serine proteinase
881	67.5	4.9	2531	2	T31070	notch homolog - se	954	66.5	4.8	576	2	T38293	hypothetical serin
882	67.5	4.9	2531	2	A46019	notch-1 protein -	955	66.5	4.8	589	2	S66856	probable membrane
883	67.5	4.9	6642	2	T29757	protein UNC-89 - C	956	66.5	4.8	589	2	S50355	alpha-glucosidase
884	67	4.9	133	2	H84217	hypothetical prote	957	66.5	4.8	598	2	S65770	maltoylglucosyltreha
885	67	4.9	163	1	A34313	antifreeze protein	958	66.5	4.8	600	2	S71949	metalloproteinase
886	67	4.9	171	1	JBAO41	chorion class B pr	959	66.5	4.8	673	2	A48089	growth arrest-spec
887	67	4.9	183	2	PN0109	keratin-like prote	960	66.5	4.8	675	2	S20819	collagen alpha 3(I
888	67	4.9	229	2	S07406	thannatin homolg	961	66.5	4.8	685	2	JC7570	Delta-4 protein -
889	67	4.9	253	2	S49158	complement protein	962	66.5	4.8	688	2	E86409	hypothetical prote
890	67	4.9	264	2	S73040	hypothetical prote	963	66.5	4.8	742	2	UC7595	seavanger receptor
891	67	4.9	272	2	S57460	cytochrome-c oxida	964	66.5	4.8	751	2	S64741	cuticle collagen -
892	67	4.9	299	2	A47031	bialaphos acetylhy	965	66.5	4.8	828	2	G82583	K-C1 cotransport p
893	67	4.9	337	2	T32164	hypothetical prote	966	66.5	4.8	1085	2	T18369	K-C1 cotransport p
894	67	4.9	336	2	H81091	probable CDP-6-deo	967	66.5	4.8	1085	2	T31429	K-C1 cotransport p
895	67	4.9	343	2	Q02372	hemagglutinin - in	968	66.5	4.8	1086	2	T14114	K-Cl cotransport p
896	67	4.9	343	2	JQ2371	hemagglutinin - in	969	66.5	4.8	1091	2	A58532	glial cell membran
897	67	4.9	344	2	PQ0321	hemagglutinin - in	970	66.5	4.8	1125	1	OYURCP	aspartic receptor p
898	67	4.9	344	2	JQ1643	hemagglutinin - in	971	66.5	4.8	2318	1	S45306	notch 3 protein -
899	67	4.9	378	2	E75621	probable chromosom	972	66.5	4.8	2471	2	A49128	cell-fate determin
900	67	4.9	401	2	AP3341	precocorrin-5r c5,15	973	66.5	4.8	2703	1	A24420	notch protein - fr
901	67	4.9	404	2	T44281	iron-sulfur cofact	974	66.5	4.8	2769	1	UIBO	thryoglobulin prec
902	67	4.9	427	2	T20800	hypothetical prote	975	66.5	4.8	2944	2	A54849	collagen alpha 1(V
903	67	4.9	456	2	D84651	hypothetical prote	976	66.5	4.8	3707	2	S18252	heparan sulfate pr
904	67	4.9	466	2	C42360	cellulase (EC 3.2.	977	66	4.8	98	2	AG1960	hypothetical prote
905	67	4.9	566	1	HMIYD1	hemagglutinin prec	978	66	4.8	170	2	AC0689	alternative bacter

979	66	4.8	238	1	LNRTMA	1052	65.5	4.8	1629	2	C84839	ferredoxin-depende
980	66	4.8	239	2	D82727	1053	65.5	4.8	2518	2	A12140	polyketide synthase
981	66	4.8	256	2	AE0997	1054	65.5	4.8	2823	2	F87908	protein T22A3.8
982	66	4.8	306	2	T21938	1055	65.5	4.8	2823	2	T23064	hypothetical prote
983	66	4.8	307	2	T18846	1056	65.5	4.8	3102	2	T43231	hypothetical prote
984	66	4.8	311	2	S48400	1057	65.5	4.8	3871	2	T22812	hypothetical prote
985	66	4.8	326	2	A35122	1058	65.5	4.8	4848	2	T30289	hypothetical prote
986	66	4.8	333	2	A35122	1059	65.5	4.8	111	2	B30289	hypothetical prote
987	66	4.8	336	2	J01437	1060	65	4.7	162	2	T49957	hypothetical prote
988	66	4.8	344	2	S41643	1061	65	4.7	181	2	T07661	ribosomal protein
989	66	4.8	344	2	P00319	1062	65	4.7	188	2	B54270	maturation protein
990	66	4.8	348	2	T29288	1063	65	4.7	229	1	S19713	insulin-like growt
991	66	4.8	353	1	D66596	1064	65	4.7	232	2	E70789	hypothetical prote
992	66	4.8	355	1	S37460	1065	65	4.7	242	2	D70625	hypothetical prote
993	66	4.8	435	2	T15143	1066	65	4.7	299	2	T20605	hypothetical prote
994	66	4.8	435	2	T15143	1067	65	4.7	303	2	S45461	hypothetical prote
995	66	4.8	553	2	T53362	1068	65	4.7	311	2	F75366	hypothetical prote
996	66	4.8	614	2	T06741	1069	65	4.7	313	2	T22828	hypothetical prote
997	66	4.8	687	2	T02459	1070	65	4.7	342	2	T22828	hypothetical prote
998	66	4.8	753	2	S35371	1071	65	4.7	349	2	T43457	hypothetical prote
999	66	4.8	854	2	T05617	1072	65	4.7	356	2	T36415	hypothetical prote
1000	66	4.8	864	2	A96574	1073	65	4.7	359	1	S28043	hypothetical prote
1001	66	4.8	1194	2	T30441	1074	65	4.7	370	2	T22810	hypothetical prote
1002	66	4.8	1364	2	C59436	1075	65	4.7	406	2	S73592	hypothetical prote
1003	66	4.8	2114	2	T09059	1076	65	4.7	416	2	H82968	hypothetical prote
1004	66	4.8	2193	2	S52919	1077	65	4.7	446	2	T34601	hypothetical prote
1005	66	4.8	3442	2	B82599	1078	65	4.7	469	2	D83861	sarcosine oxidase
1006	66	4.8	3455	2	B82519	1079	65	4.7	476	2	T10711	probable funarylac
1007	66	4.8	3507	2	T34513	1080	65	4.7	619	2	T29054	hypothetical prote
1008	66	4.8	37	2	S03570	1081	65	4.7	711	2	D86296	probable DNA repa
1009	65.5	4.8	97	2	S26598	1082	65	4.7	715	2	S52675	hypothetical prote
1010	65.5	4.8	114	2	T74627	1083	65	4.7	737	2	T02178	hypothetical prote
1011	65.5	4.8	114	2	T74627	1084	65	4.7	759	2	T44142	hypothetical prote
1012	65.5	4.8	140	2	S78593	1085	65	4.7	826	2	J00317	hypothetical prote
1013	65.5	4.8	147	2	A84546	1086	65	4.7	866	2	S57936	hypothetical prote
1014	65.5	4.8	202	2	T35703	1087	65	4.7	881	2	T49379	hypothetical prote
1015	65.5	4.8	228	2	T35703	1088	65	4.7	884	2	T00326	hypothetical prote
1016	65.5	4.8	245	1	C1H0UA	1089	65	4.7	1112	1	DNBK5	hypothetical prote
1017	65.5	4.8	286	2	T15524	1090	65	4.7	1137	2	T10129	hypothetical prote
1018	65.5	4.8	298	2	T27644	1091	65	4.7	1374	2	T02087	hypothetical prote
1019	65.5	4.8	304	2	JC5845	1092	65	4.7	1439	2	D70807	hypothetical prote
1020	65.5	4.8	311	2	B85845	1093	65	4.7	1522	2	T00807	hypothetical prote
1021	65.5	4.8	311	2	D91023	1094	65	4.7	1603	1	BVSA1	hypothetical prote
1022	65.5	4.8	327	2	AG3367	1095	65	4.7	1707	2	A33526	3-dehydroquinate s
1023	65.5	4.8	327	2	S63248	1096	65	4.7	1901	2	F70806	collagen alpha 2(I
1024	65.5	4.8	350	2	T37285	1097	65	4.7	2083	2	T42721	hypothetical glyci
1025	65.5	4.8	363	2	T16831	1098	65	4.7	2166	2	S11339	calcium channel pr
1026	65.5	4.8	371	2	B72461	1099	65	4.7	2171	2	S05054	CRP-ductin-alpha p
1027	65.5	4.8	396	2	T29273	1100	65	4.7	2244	2	T08212	RNA-directed RNA p
1028	65.5	4.8	397	2	S28274	1101	65	4.7	2284	2	T67630	surface protein ty
1029	65.5	4.8	402	1	CGR025	1102	65	4.7	2395	1	S50820	protein-tyrosine-p
1030	65.5	4.8	452	1	T30082	1103	65	4.7	2466	1	A54971	lactyl-acid synthas
1031	65.5	4.8	467	1	WZB661	1104	65	4.7	2509	2	G01880	gamma-F-cryofallin
1032	65.5	4.8	479	2	C94957	1105	65	4.7	2509	2	A34493	collagen alpha 1(I
1033	65.5	4.8	488	2	A27353	1106	65	4.7	2509	2	A34493	collagen alpha 1(I
1034	65.5	4.8	576	2	S33327	1107	65	4.7	2509	2	A34493	collagen alpha 1(I
1035	65.5	4.8	615	2	A05269	1108	65	4.7	2509	2	A34493	collagen alpha 1(I
1036	65.5	4.8	691	2	A54741	1109	65	4.7	2509	2	A34493	collagen alpha 1(I
1037	65.5	4.8	730	2	A54741	1110	65	4.7	2509	2	A34493	collagen alpha 1(I
1038	65.5	4.8	741	2	A54741	1111	65	4.7	2509	2	A34493	collagen alpha 1(I
1039	65.5	4.8	741	2	A54741	1112	65	4.7	2509	2	A34493	collagen alpha 1(I
1040	65.5	4.8	752	2	A54741	1113	65	4.7	2509	2	A34493	collagen alpha 1(I
1041	65.5	4.8	775	2	A54741	1114	65	4.7	2509	2	A34493	collagen alpha 1(I
1042	65.5	4.8	877	2	B83966	1115	65	4.7	2509	2	A34493	collagen alpha 1(I
1043	65.5	4.8	877	2	B83966	1116	65	4.7	2509	2	A34493	collagen alpha 1(I
1044	65.5	4.8	947	2	T23107	1117	65	4.7	2509	2	A34493	collagen alpha 1(I
1045	65.5	4.8	966	1	PIBVB8	1118	65	4.7	2509	2	A34493	collagen alpha 1(I
1046	65.5	4.8	969	2	B87083	1119	65	4.7	2509	2	A34493	collagen alpha 1(I
1047	65.5	4.8	1137	2	T02097	1120	65	4.7	2509	2	A34493	collagen alpha 1(I
1048	65.5	4.8	1140	1	GOHUE	1121	65	4.7	2509	2	A34493	collagen alpha 1(I
1049	65.5	4.8	1195	2	A32901	1122	65	4.7	2509	2	A34493	collagen alpha 1(I
1050	65.5	4.8	1353	1	J02168	1123	65	4.7	2509	2	A34493	collagen alpha 1(I
1051	65.5	4.8	1360	2	T33922	1124	65	4.7	2509	2	A34493	collagen alpha 1(I
	4.8	1376	1	J01534								
	4.8	1492	2	A40334								

1125	64.5	4.7	242	2	S60143	cellulase (EC 3.2.	1198	64	4.7	426	2	D88103	protein W10G11.6 [
1126	64.5	4.7	262	2	A54889	IgE-binding protei	1199	64	4.7	465	1	S47738	cytochrome-c perox
1127	64.5	4.7	266	2	T22706	hypothetical prote	1200	64	4.7	465	2	P91178	cytochrome-c perox
1128	64.5	4.7	277	1	Q08BC2	HKRFx protein - hu	1201	64	4.7	465	2	G86024	hypothetical prote
1129	64.5	4.7	297	2	T27525	hypothetical prote	1202	64	4.7	487	2	T15923	hypothetical prote
1130	64.5	4.7	301	2	B31219	collagen 2 - Caeno	1203	64	4.7	502	2	S36526	L1 protein - human
1131	64.5	4.7	317	2	T29960	hypothetical prote	1204	64	4.7	504	2	S56745	cellulose 1,4-beta
1132	64.5	4.7	318	2	S27977	cuticle collagen d	1205	64	4.7	516	2	S42093	hemagglutinin prec
1133	64.5	4.7	328	2	AD1916	alcohol dehydrogen	1206	64	4.7	566	1	HMIYR	hemagglutinin prec
1134	64.5	4.7	333	2	T15867	hypothetical prote	1207	64	4.7	566	2	S69888	hemagglutinin prec
1135	64.5	4.7	334	2	B75400	phosphoribosylform	1208	64	4.7	595	2	P95379	probable adenine d
1136	64.5	4.7	356	2	T05119	leucanthocyanidin	1209	64	4.7	663	1	S18572	tetracycline resis
1137	64.5	4.7	387	2	E95933	probable calcium-b	1210	64	4.7	669	2	A5103	cell surface recep
1138	64.5	4.7	398	2	B71284	probable periplasm	1211	64	4.7	697	2	T37946	tryptophan synthas
1139	64.5	4.7	411	2	B91220	probable arylsulfa	1212	64	4.7	717	2	T49238	hypothetical prote
1140	64.5	4.7	411	2	D86066	probable arylsulfa	1213	64	4.7	719	2	A87292	primosomal protein
1141	64.5	4.7	411	2	S58105	Cu metalloregulato	1214	64	4.7	721	2	F70649	probable Acyl-CoA
1142	64.5	4.7	416	2	T41665	probable dipeptida	1215	64	4.7	728	2	I50719	C-Delta-1 - chick
1143	64.5	4.7	445	2	D86620	phosphoshikimate v	1216	64	4.7	753	2	AH0097	probable biotin su
1144	64.5	4.7	445	2	C72004	phosphoshikimate v	1217	64	4.7	823	2	T21104	hypothetical prote
1145	64.5	4.7	460	1	Q0RT	hemopexin precursor	1218	64	4.7	843	2	T13334	probable tail-host
1146	64.5	4.7	529	2	S36578	L1 protein - human	1219	64	4.7	861	2	B98847	nitrate reductase
1147	64.5	4.7	532	2	AE1964	Dnak-type molecula	1220	64	4.7	895	2	AD0541	outer membrane fim
1148	64.5	4.7	547	1	A32244	60X cysteine-rich	1221	64	4.7	963	2	T19140	hypothetical prote
1149	64.5	4.7	553	2	D71515	60X cysteine-rich	1222	64	4.7	998	2	T35745	probable ATP-bind
1150	64.5	4.7	562	2	A85524	choline dehydrogen	1223	64	4.7	1000	2	AB3467	sarcosine oxidase
1151	64.5	4.7	562	2	E90673	choline dehydrogen	1224	64	4.7	1083	2	H86921	probable arabinosy
1152	64.5	4.7	570	2	S42708	proline transport	1225	64	4.7	1955	1	AGCH	agrin precursor -
1153	64.5	4.7	570	2	S04547	proline transport	1226	64	4.7	2042	2	T18399	variant-specific B
1154	64.5	4.7	597	2	JC7615	alpha-glucosidase	1227	64	4.7	2321	2	S78549	notch3 protein - h
1155	64.5	4.7	599	2	T25835	hypothetical prote	1228	64	4.7	3137	2	A37797	collagen alpha 3(V
1156	64.5	4.7	618	2	S32436	collagen alpha 2(I	1229	64	4.7	3461	2	S58870	reelin precursor -
1157	64.5	4.7	626	2	C72035	succinate dehydrog	1230	64	4.7	3635	2	T10053	laminin alpha 5 ch
1158	64.5	4.7	626	2	C86589	succinate dehydrog	1231	64	4.7	7463	2	T36248	CD4 peptide synthe
1159	64.5	4.7	644	2	JC2346	kexin-like protein	1232	63.5	4.6	97	2	G34964	Ig heavy chain V-I
1160	64.5	4.7	646	2	H96665	protein F22C12.10	1233	63.5	4.6	144	2	S24805	hypothetical prote
1161	64.5	4.7	651	1	S23667	cytochrome c-type	1234	63.5	4.6	152	2	T24064	hypothetical prote
1162	64.5	4.7	653	2	T02080	probable carbonate	1235	63.5	4.6	184	2	D83234	hypothetical prote
1163	64.5	4.7	666	2	F71310	probable periplasm	1236	63.5	4.6	191	2	L64412	keratin KAP5.4 - 8
1164	64.5	4.7	678	2	B84856	hypothetical prote	1237	63.5	4.6	191	2	AF0580	lipocate-protein 11
1165	64.5	4.7	715	2	S70397	zona pellucida gly	1238	63.5	4.6	215	2	AD0455	thiamine-phosphate
1166	64.5	4.7	721	2	C84732	probable homeodoma	1239	63.5	4.6	220	2	S35789	US2 protein - bovi
1167	64.5	4.7	724	2	C71274	hypothetical prote	1240	63.5	4.6	232	1	TLBPUL	minor tail protein
1168	64.5	4.7	730	2	H86295	hypothetical prote	1241	63.5	4.6	234	1	T31753	hypothetical prote
1169	64.5	4.7	884	2	S61569	hypothetical prote	1242	63.5	4.6	253	1	C1H0UB	complement subcomp
1170	64.5	4.7	1374	1	GANNYC	genome polyprotein	1243	63.5	4.6	256	2	T28853	hypothetical prote
1171	64.5	4.7	1376	1	VG1HJ2	E2 glycoprotein pr	1244	63.5	4.6	269	2	C83516	hypothetical prote
1172	64.5	4.7	1388	2	A53317	collagen alpha 1(X	1245	63.5	4.6	281	2	T32765	hypothetical prote
1173	64.5	4.7	1408	2	S16148	gene serrate prote	1246	63.5	4.6	281	2	C88638	protein F58Fe.1 [I
1174	64.5	4.7	1487	2	T02850	hypothetical prote	1247	63.5	4.6	289	2	T34241	hypothetical prote
1175	64.5	4.7	1546	1	CGHJ2B	collagen alpha 2(X	1248	63.5	4.6	289	2	T26812	hypothetical prote
1176	64.5	4.7	1712	1	CGHJ2B	collagen alpha 2(I	1249	63.5	4.6	290	2	A32249	collagen - sea urc
1177	64.5	4.7	2139	2	A35672	intrinsc factor - B	1250	63.5	4.6	291	2	T34494	hypothetical prote
1178	64.5	4.7	3623	2	T09456	T-cell receptor al	1251	63.5	4.6	294	2	T33916	hypothetical prote
1179	64	4.7	104	2	JH0345	hisactophilin [val	1252	63.5	4.6	308	2	H90452	conserved hypotnet
1180	64	4.7	118	1	A31429	keratin, claw - ch	1253	63.5	4.6	311	2	B64988	hypothetical prote
1181	64	4.7	128	2	Q01002	Ig heavy chain V r	1254	63.5	4.6	316	2	T20497	hypothetical prote
1182	64	4.7	133	2	B38911	osmotic protein ho	1255	63.5	4.6	320	2	C81029	3-oxoacyl-(acyl-ac
1183	64	4.7	218	2	T03287	phosphoribosylform	1256	63.5	4.6	320	2	T39110	probable gtpase ac
1184	64	4.7	238	2	B75266	pulmonary surfacta	1257	63.5	4.6	326	2	T02340	GTP-binding regula
1185	64	4.7	248	1	LNHJ26	integral membrane	1258	63.5	4.6	328	2	T16970	conserved hypotnet
1186	64	4.7	278	2	C43670	hypothetical prote	1259	63.5	4.6	335	2	A40038	MHC class I histoc
1187	64	4.7	304	2	T23801	hypothetical prote	1260	63.5	4.6	338	2	T49182	probable chloropla
1188	64	4.7	310	2	T29731	hypothetical prote	1261	63.5	4.6	357	2	H75541	probable oxidoredu
1189	64	4.7	333	2	T50630	8-hydroxy-guanine	1262	63.5	4.6	371	2	E88633	protein F56B3.1 [I
1190	64	4.7	346	2	T45069	glycoprotein D pre	1263	63.5	4.6	375	2	A95867	conserved pyrrolou
1191	64	4.7	394	1	VGEB17	glycoprotein F25B5.10	1264	63.5	4.6	378	2	AB0894	conserved hypotnet
1192	64	4.7	401	2	CG9102	glutamate dehydrog	1265	63.5	4.6	388	2	T27806	hypothetical prote
1193	64	4.7	411	2	T16982	glutamate dehydrog	1266	63.5	4.6	404	2	T40553	hypothetical prote
1194	64	4.7	411	2	T04342	glutamate dehydrog	1267	63.5	4.6	418	2	S31124	conserved hypotnet
1195	64	4.7	411	2	T03294	hypothetical prote	1268	63.5	4.6	435	2	B87412	probable amidase A
1196	64	4.7	426	2	AH2144		1269	63.5	4.6	445	2	C72695	
1197	64	4.7	426	2			1270	63.5	4.6				

1271	63.5	4.6	481	2	A33712	metallopeptidase	1344	63	4.6	437	2	UC7138	alpha-amylase (EC
1272	63.5	4.6	498	2	B84789	probable protein w	1345	63	4.6	437	2	UT0946	alpha-amylase 3B -
1273	63.5	4.6	504	1	PIW131	Li protein - human	1346	63	4.6	438	2	D88206	protein nhr-21.a [
1274	63.5	4.6	538	2	S65764	chitinase (EC 3.2.	1347	63	4.6	453	2	A71891	glu-tRNA amidoran
1275	63.5	4.6	556	1	SI0901	choline dehydrogen	1348	63	4.6	453	2	AE2955	glutamy1-tRNA amid
1276	63.5	4.6	654	2	A34734	transcription fact	1349	63	4.6	471	2	A39024	collagen alpha 3(I
1277	63.5	4.6	660	2	C90343	conserved hypothet	1350	63	4.6	475	2	AB0855	conserved hypothet
1278	63.5	4.6	680	2	T25832	hypothetical prote	1351	63	4.6	475	2	H91077	probable 4-hydroxy
1279	63.5	4.6	690	2	T08604	hypothetical prote	1352	63	4.6	475	2	T44997	probable 4-hydroxy
1280	63.5	4.6	700	2	T41401	sprote outgrowth fa	1353	63	4.6	475	2	A85923	probable 4-hydroxy
1281	63.5	4.6	724	2	D87530	isoquinoline 1-oxi	1354	63	4.6	480	2	F70785	hypothetical prote
1282	63.5	4.6	728	2	S26427	transcriptional pro	1355	63	4.6	487	2	T21384	hypothetical prote
1283	63.5	4.6	742	4	C34734	P-selectin precurs	1356	63	4.6	513	1	EUT01	cellulose 1,4-beta
1284	63.5	4.6	768	2	A42755	probable type II s	1357	63	4.6	513	2	S45380	cellulose 1,4-beta
1285	63.5	4.6	803	2	C83561	transcription fact	1358	63	4.6	543	2	H82282	vibriobactin-speci
1286	63.5	4.6	825	4	B34734	Cooc protein precu	1359	63	4.6	545	2	T02079	probable carbonate
1287	63.5	4.6	872	2	S45358	potassium channel	1360	63	4.6	582	2	SI0059	transcription fact
1288	63.5	4.6	883	2	T07651	receptor kinase ho	1361	63	4.6	611	2	T27013	hypothetical prote
1289	63.5	4.6	901	2	T04108	hypothetical prote	1362	63	4.6	632	2	T27155	hypothetical prote
1290	63.5	4.6	907	2	T15792	PACRA - mouse (fr	1363	63	4.6	633	2	B40983	collagen alpha 1(X
1291	63.5	4.6	932	2	I52527	hypothetical prote	1364	63	4.6	633	2	T27155	cytokeratin 2 - hu
1292	63.5	4.6	1042	2	T26644	hypothetical prote	1365	63	4.6	638	2	I53169	glucose inhibited
1293	63.5	4.6	1345	2	S46817	hypothetical prote	1366	63	4.6	658	2	AB3253	hypothetical prote
1294	63.5	4.6	1381	2	E70806	hypothetical glyci	1367	63	4.6	684	2	F83375	translation elonga
1295	63.5	4.6	1549	2	I48103	type VII collagen	1368	63	4.6	692	2	B69628	translation elonga
1296	63.5	4.6	1573	2	S01845	DNA (cytosine-5-)-	1369	63	4.6	692	2	C83666	translation elonga
1297	63.5	4.6	1649	2	C86822	hypothetical prote	1370	63	4.6	692	2	T44380	translation elonga
1298	63.5	4.6	1693	2	S76086	beta transducin-11	1371	63	4.6	695	2	AE1782	translation elonga
1299	63.5	4.6	1959	1	AGRT	argin - rat	1372	63	4.6	695	2	AE1782	translation elonga
1300	63.5	4.6	2185	1	GNNYBT	genome polyprotein	1373	63	4.6	705	2	G87316	translation elonga
1301	63.5	4.6	2185	1	UQ2021	genome polyprotein	1374	63	4.6	760	2	A45174	translation elonga
1302	63.5	4.6	2195	2	T34264	hypothetical prote	1375	63	4.6	946	2	T16297	translation elonga
1303	63.5	4.6	2352	2	T30201	Notch homolog prot	1376	63	4.6	1125	1	S57846	translation elonga
1304	63.5	4.6	2533	2	T28675	alpha-51D immobili	1377	63	4.6	1125	1	S57846	translation elonga
1305	63.5	4.6	2533	2	T28674	alpha-51D-immobili	1378	63	4.6	1170	2	A53612	translation elonga
1306	63.5	4.6	3063	2	S55505	fatty-acid synthas	1379	63	4.6	1203	2	A49175	translation elonga
1307	63.5	4.6	3429	2	T13853	hypothetical prote	1380	63	4.6	1331	2	T18310	translation elonga
1308	63	4.6	40	2	A49081	capillary permeabi	1381	63	4.6	1367	2	S55669	translation elonga
1309	63	4.6	99	2	S26801	early chorion prot	1382	63	4.6	1367	2	T33819	translation elonga
1310	63	4.6	119	2	B45937	chorion protein -	1383	63	4.6	1820	2	A55494	translation elonga
1311	63	4.6	119	2	S24294	hypothetical prote	1384	63	4.6	2157	1	GNNY1B	translation elonga
1312	63	4.6	192	2	A83153	hypothetical prote	1385	63	4.6	2437	2	S42612	translation elonga
1313	63	4.6	212	2	B66179	collagen UC0L1 - p	1386	63	4.6	2647	2	A37098	translation elonga
1314	63	4.6	228	2	A44982	probable phosdoc	1387	63	4.6	3176	2	CGH03A	translation elonga
1315	63	4.6	240	1	F70631	probable phosdoc	1388	62.5	4.5	118	2	S29653	translation elonga
1316	63	4.6	242	1	F75433	complement subcomp	1389	62.5	4.5	144	2	S01391	translation elonga
1317	63	4.6	245	1	CIHUOC	pulmonary surfacta	1390	62.5	4.5	155	2	C44012	translation elonga
1318	63	4.6	248	1	LNHUPS	hypothetical prote	1391	62.5	4.5	165	2	S72776	translation elonga
1319	63	4.6	257	2	T28946	cob(1)alamin adeno	1392	62.5	4.5	181	2	A70627	translation elonga
1320	63	4.6	265	2	AG0814	hypothetical prote	1393	62.5	4.5	198	2	I49558	translation elonga
1321	63	4.6	269	2	S36166	paired box transcr	1394	62.5	4.5	214	2	T18539	translation elonga
1322	63	4.6	285	2	T29982	hypothetical prote	1395	62.5	4.5	222	2	B23746	translation elonga
1323	63	4.6	299	2	T24833	hypothetical prote	1396	62.5	4.5	231	2	S33197	translation elonga
1324	63	4.6	302	2	T15936	hypothetical prote	1397	62.5	4.5	247	2	H81036	translation elonga
1325	63	4.6	303	2	E86591	CT580 hypothetical	1398	62.5	4.5	299	2	T29956	translation elonga
1326	63	4.6	308	2	D72031	neurosporene hydro	1399	62.5	4.5	306	2	H81036	translation elonga
1327	63	4.6	309	2	S32172	hypothetical prote	1400	62.5	4.5	313	2	T33010	translation elonga
1328	63	4.6	308	2	B69995	probable 3-oxocacyl	1401	62.5	4.5	316	2	T19288	translation elonga
1329	63	4.6	320	2	C81972	collagen col-14 -	1402	62.5	4.5	341	2	F70625	translation elonga
1330	63	4.6	326	2	JS0169	hypothetical prote	1403	62.5	4.5	352	2	F70625	translation elonga
1331	63	4.6	348	2	T28623	hypothetical prote	1404	62.5	4.5	356	2	SB0296	translation elonga
1332	63	4.6	349	2	D36858	gene G4R protein -	1405	62.5	4.5	359	2	T22774	translation elonga
1333	63	4.6	357	1	S33321	glutamy1 endopepti	1406	62.5	4.5	391	2	F87258	translation elonga
1334	63	4.6	369	2	S33603	surfactant protein	1407	62.5	4.5	398	2	AG0128	translation elonga
1335	63	4.6	400	2	A83518	hypothetical prote	1408	62.5	4.5	398	2	T35255	translation elonga
1336	63	4.6	403	2	C75336	serine proteinase,	1409	62.5	4.5	402	2	S37789	translation elonga
1337	63	4.6	403	2	H98327	enantiomer-selecti	1410	62.5	4.5	411	2	S71217	translation elonga
1338	63	4.6	418	2	T15142	hypothetical prote	1411	62.5	4.5	427	2	S75210	translation elonga
1339	63	4.6	422	1	A56674	paired box transcr	1412	62.5	4.5	450	2	E70681	translation elonga
1340	63	4.6	424	2	C86477	hypothetical prote	1413	62.5	4.5	466	2	A87638	translation elonga
1341	63	4.6	428	2	T27544	zinc resistance pr	1414	62.5	4.5	473	2	A56175	translation elonga
1342	63	4.6	434	2	D96760	hypothetical prote	1415	62.5	4.5	478	2	S31906	translation elonga
1343	63	4.6	436	1	S42234	paired box transcr	1416	62.5	4.5	482	2	S76376	translation elonga

1417	62.5	4.5	498	2	A72725	probable beta-lact
1418	62.5	4.5	532	2	T49824	hypothetical prote
1419	62.5	4.5	560	2	T16833	hypothetical prote
1420	62.5	4.5	561	2	A84287	hypothetical prote
1421	62.5	4.5	577	2	A60501	thrombomodulin pre
1422	62.5	4.5	589	2	T29299	hypothetical prote
1423	62.5	4.5	612	2	S53714	probable dinitrifi
1424	62.5	4.5	678	2	B48089	growth arrest-spec
1425	62.5	4.5	684	2	A53019	collagen alpha 1(X
1426	62.5	4.5	695	2	E71463	probable polyribon
1427	62.5	4.5	709	2	S33907	glycerol kinase (E
1428	62.5	4.5	722	2	148324	DELTA-like 1 - mou
1429	62.5	4.5	731	2	JC7701	ARHGAP9 protein -
1430	62.5	4.5	784	2	A26601	elastin precursor
1431	62.5	4.5	799	2	A38308	integrin beta-5 ch
1432	62.5	4.5	810	2	C84845	probable salt-indu
1433	62.5	4.5	979	2	D96574	hypothetical prote
1434	62.5	4.5	1030	2	H96568	unknown protein, 2
1435	62.5	4.5	1039	2	A41131	lymphocyte-Peyer's
1436	62.5	4.5	1107	2	T15884	hypothetical prote
1437	62.5	4.5	1160	2	F88369	protein unc-52 (im
1438	62.5	4.5	1257	2	S28764	neurocan precursor
1439	62.5	4.5	1308	2	A47253	epidermal growth f
1440	62.5	4.5	1610	2	A46227	voltage-dependent
1441	62.5	4.5	1646	2	JH0422	voltage-dependent
1442	62.5	4.5	2203	2	T42742	voltage-dependent
1443	62.5	4.5	2295	2	C88359	protein unc-52 (im
1444	62.5	4.5	2491	1	A28312	insulin-like growt
1445	62.5	4.5	2591	2	T30288	pristnamycin I sy
1446	62.5	4.5	3375	2	T19821	hypothetical prote
1447	62	4.5	43	2	A61168	cocoonase (EC 3.4.
1448	62	4.5	98	2	S39410	noar protein - Par
1449	62	4.5	99	2	S26807	Ig heavy chain V r
1450	62	4.5	99	2	S26800	Ig heavy chain V r
1451	62	4.5	137	2	B72679	hypothetical prote
1452	62	4.5	161	2	A46189	vasococin - Pacifi
1453	62	4.5	208	2	E82670	general secretory
1454	62	4.5	215	2	C48150	hibernation-relate
1455	62	4.5	237	2	T16285	hypothetical prote
1456	62	4.5	240	2	S30406	hypothetical prote
1457	62	4.5	247	2	T35602	probable transposa
1458	62	4.5	283	2	T19731	hypothetical prote
1459	62	4.5	283	2	T19732	hypothetical prote
1460	62	4.5	283	2	T29980	hypothetical prote
1461	62	4.5	286	2	C87380	conserved hypochet
1462	62	4.5	298	2	A40289	probable aldo/keto
1463	62	4.5	299	2	A96655	protein P22C12.24
1464	62	4.5	299	2	S68198	probable transcrip
1465	62	4.5	302	2	T21257	hypothetical prote
1466	62	4.5	308	2	T19846	hypothetical prote
1467	62	4.5	317	2	T19143	hypothetical prote
1468	62	4.5	327	2	T34203	hypothetical prote
1469	62	4.5	328	2	G64901	ABC-type transport
1470	62	4.5	330	2	S08500	OUTG protein - Eme
1471	62	4.5	336	2	F81849	probable CDP-6-deo
1472	62	4.5	336	2	A35160	repressor protein
1473	62	4.5	336	2	T20348	hypothetical prote
1474	62	4.5	342	2	A46529	Ig gamma chain (5.
1475	62	4.5	347	2	AC1813	IMP dehydrogenase
1476	62	4.5	393	1	VGBEDZ	glycoprotein D pre
1477	62	4.5	399	2	F82657	beta-ketocacyl- (AC
1478	62	4.5	401	2	B64598	tetracyclodipicoli
1479	62	4.5	401	2	E82951	probable MFS trans
1480	62	4.5	416	2	S48957	hypothetical prote
1481	62	4.5	426	2	H84349	peroxidase / catal
1482	62	4.5	446	2	D70597	probable signal pe
1483	62	4.5	456	2	C96684	fl2p19.15 (importe
1484	62	4.5	462	2	T24565	capsid protein 22
1485	62	4.5	468	2	A69468	ammonium transport
1486	62	4.5	502	2	A12868	phosphomannomutase
1487	62	4.5	502	2	JE0295	Li protein - human
1488	62	4.5	506	2	C97645	phosphomannomutase
1489	62	4.5	508	2	G84339	phosphoglycerate m

1490	62	4.5	552	2	C86171	hypothetical prote
1491	62	4.5	566	2	S69899	hemagglutinin prec
1492	62	4.5	567	2	AC0885	hydrogenase-2 larg
1493	62	4.5	589	2	B38128	epithelin/granulin
1494	62	4.5	591	2	B70523	hypothetical glyci
1495	62	4.5	592	2	JN0877	protein kinase C (
1496	62	4.5	606	2	T51880	hypothetical prote
1497	62	4.5	628	2	AB0548	PP2B protein (limp
1498	62	4.5	651	2	JC7705	death receptor-6-
1499	62	4.5	670	2	S22293	zinc finger protei
1500	62	4.5	693	2	E89622	translational elon

ALIGNMENTS

RESULT 1
156559
neuropilin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 156559
R/Chen, Z.-L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishim
J. Neurosci. 15, 5088-5097, 1995
A>Title: Expression and activity-dependent changes of a novel limbic-serine protease gen
A/Reference number: 156559; MUID:95348817; PMID:7623117
A/Accession: 156559
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-260 <RES>
A/Cross-references: UNIPROT:O61955; GB:D30785; NID:G1648847; PIDN:BAA06451.1; PID:G102001
C/Superfamily: trypsin; trypsin homology
F_33-252/Domain: trypsin homology <TRX>

Query Match 45.3%; Score 622.5; DB 2; Length 260;
Best Local Similarity 49.0%; Pred. No. 3.2e-43;
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

QY	5	IFLLLCV---LGLSQATPKIFNTEGCRNSQPPQVLFEFTSLRCGGVLDHNVLTAA	61
DB	13	ILLFLFGAWAGLTRAQGSKILEREICIPHSQPQALFGSERLICGVLVGRWVLTAA	72
QY	62	HCGSGRYWVRLGSHSLQDLMTBQIRHSGSVTHPGVLGAS-TSHEHDLRLRLPVRV	120
DB	73	HCKKQKTSVRLGSHSLQDLMTBQIRHSGSVTHPGVLGAS-TSHEHDLRLRLPVRV	132
QY	121	TSSVQPLPLPNDCACTAGTECHSVSGWGITNHPNPFDDLLQCLNLSIVSHATCHGVPGRI	180
DB	133	GDKVKPVLQANLCPKVKQKICISGQWTVTSPOENFPVTLNCAEVKISQNKCEAATGKI	192
QY	181	TSNNVCAGVPGDACCDSGGSPLYCGVULQGLVSGSVGPGCGDGIPTVYTYICXVVDW	240
DB	193	TEGVNVCAGSNGADTCGDSGSPVCDGMLOGITSMGS-DPCGKPEKPGVYTKICRYTWW	251
QY	241	IRIMIMRV 247	
DB	252	IKKTMVN 258	

RESULT 2
S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N/Alternate names: trypsinogen II
C/Species: Gallus gallus (chicken)
C/Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
A/Accession: S55066; S72347
R/Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A>Title: Isolation and characterization of the chicken trypsinogen gene family.
A/Reference number: S55065; MUID:95251611; PMID:7733885
A/Accession: S55066
A/Molecule type: mRNA
A/Residues: 1-248 <MAN1>

A/Cross-references: UNIPROT:Q90629; EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603903
A/Experimental source: clone 2-P29
A/Accession: S72347
A/Molecule type: DNA
A/Residues: 1-248 <MAN2>
A/Cross-references: EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603907
A/Experimental source: clone 2-P29
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F/1-16/Domain: signal sequence #status predicted <SIG>
F/17-25/Domain: activation peptide #status predicted <APR>
F/26-248/Product: trypsin II #status predicted <MAT>
F/26-241/Domain: trypsin homology <TRY>
F/65,109,202/Active site: His, Asp, Ser #status predicted

Query Match 41.4%; Score 569.5; DB 2; Length 248;
Best Local Similarity 47.5%; Pred. No. 66-39;
Matches 116; Conservative 39; Mismatches 78; Indels 11; Gaps 6;
QY 5 ILLLCVGLS-----QAATPKIFNGTECGRNSQPMOVGLFEGTSLRCGVLIDHRWLT 59
Db 4 LFLILSCGAANAFAFGADDDKIVGGYTCPEHSVYQVSLNSGYHF-CGGSILNSQWLS 62
QY 60 AAHCGSRVWVRLGSHLSQLDWTEQIRHSGFVTHPGYLGASTSHHDRLRLRL 119
Db 63 AAHCKSRIOVRLGEVNIIDVQEDSEVNSSVYIIRPKY--SSITLNDIMLIKASAVE 120
QY 120 VTSSVQPLPLPNDCAATAGTECHVSGWGITNHRNFPDILLOCLNLSIVSHATCGVYGR 179
Db 121 YSADIQPLALPSSCAKAGTECLISGMNTLSNGVYPELLQCLNAPILSDCEQEAIFGD 180
QY 180 ITSNMVCAGVPL-GODACQDSGSGPLVCGVYLQGLVSGSVGPCGQDGIPEVYTYIC 238
Db 181 ITSNMTCVFLBGGKDSQCGDSGPGVVCNGLQGLVSWG-IG-CALKGYPGVYTKVCNV 238
QY 239 DWIR 242
Db 239 DWIQ 242

RESULT 3

trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken
N/Alternate names: trypsinogen I
C/Species: Gallus gallus (chicken)
C/Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
C/Accession: S55067; S72345; S55065; S72346; S71155
R/Wang, K.; Gan, L.; Lee, I.; Hood, L.
A/Title: Isolation and characterization of the chicken trypsinogen gene family.
A/Reference number: S55065; MUID:95251611; PMID:7733885
A/Accession: S55067
A/Molecule type: mRNA
A/Residues: 1-248 <MAN1>
A/Cross-references: UNIPROT:Q90627; UNIPROT:Q90628; EMBL:U15156; NID:g603904
A/Experimental source: clone 1-P38
A/Accession: S72345
A/Molecule type: DNA
A/Residues: 1-248 <MAN2>
A/Experimental source: clone 1-P38
A/Accession: S55065
A/Molecule type: mRNA
A/Residues: 1-9, 'V', '11-12, 'T', '14-102, 'A', '104-214, 'I', '216-248 <MAN3>
A/Cross-references: EMBL:U15155; NID:g603902; PIDN:AAA79912.1; PID:g603903
A/Experimental source: clone 1-P1
A/Accession: S72346
A/Molecule type: DNA
A/Residues: 1-9, 'V', '11-12, 'T', '14-102, 'A', '104-214, 'I', '216-248 <MAN4>
A/Cross-references: GB:U15155; NID:g603902; PIDN:AAA79912.1; PID:g603903
R/Wang, K.
submitted to the EMBL Data Library, September 1994
A/Reference number: S71155

A/Accession: S71155
A/Molecule type: mRNA
A/Residues: 1-102, 'A', '104-248 <MAN5>
A/Cross-references: EMBL:U15156; NID:g603904; PIDN:AAA79913.1; PID:g603905
A/Experimental source: clone 1-P38
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F/1-15/Domain: signal sequence #status predicted <SIG>
F/16-25/Domain: activation peptide #status predicted <APR>
F/26-248/Product: trypsin I #status predicted <MAT>
F/26-241/Domain: trypsin homology <TRY>
F/65,109,202/Active site: His, Asp, Ser #status predicted

Query Match 41.3%; Score 567.7; DB 2; Length 248;
Best Local Similarity 45.8%; Pred. No. 9.66-39;
Matches 115; Conservative 38; Mismatches 88; Indels 12; Gaps 6;
QY 3 LSLFLLCVLG-----LSQAATPKIFNGTECGRNSQPMOVGLFEGTSLRCGVLIDHRW 56
Db 1 MKFLVLAFLGVAVAPPISEDDDKIVGGYSCARSAAPQVSLNSGYHF-CGGSILNSQW 59
QY 57 VLTAAHCGSRVWVRLGSHLSQLDWTEQIRHSGFVTHPGYLGASTSHHDRLRLRL 116
Db 60 VLSAAHCKYSSIQVKLGEVNLAAQDSQETISSKVIIRHSY--NSNTLNDIMLIKASAVE 117
QY 117 PVARVTSVQPLPLPNDCAATAGTECHVSGWGITNHRNFPDILLOCLNLSIVSHATCGVY 176
Db 118 AALINAVYVTVPLPISCTTAGITCLISGMNTLSGSLVDPVLOCLNAPVLSQCSAY 177
QY 177 PGRITSNMVCAGVPL-PGQDACQDSGSGPLVCGVYLQGLVSGSVGPCGQDGIPEVYTYIC 235
Db 178 PGRITSNMTCVFLBGGKDSQCGDSGPGVVCNGLQGLVSWG-IG-CALKGYPGVYTKVCNV 235
QY 236 KYVDWIR 248
Db 236 NYVSWIKTKTSSN 248

RESULT 4

trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)
N/Contains: trypsinogen
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 09-Jul-2004
C/Accession: A90641; A90368; A00947
R/Charles, M.; Roversy, M.; Guidoni, A.; Desnuelle, P.
A/Title: Su le trypsinogene et la trypsine de porc.
A/Reference number: A90641
A/Accession: A90641
A/Molecule type: protein
A/Residues: 1-10 <CHA>
A/Cross-references: UNIPROT:P00761
B/Hermanson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.
A/Title: Determination of the amino acid sequence of porcine trypsin by sequenator analy
A/Reference number: A90368; MUID:73258692; PMID:4738933
A/Accession: A90368
A/Molecule type: protein
A/Residues: 9-231 <HER>
A/Note: at position 20, Ile and Val occur alternatively
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; zym
F/1-231/Product: trypsinogen #status experimental <ZYM>
F/1-8/Domain: activation peptide #status experimental <APR>
F/9-231/Product: trypsin homology <TRY>
F/9-224/Domain: trypsin homology <TRY>
F/15-145,33-49,117-218,124-191,155-170,181-205/Disulfide bonds: #status predicted
F/48,92,185/Active site: His, Asp, Ser #status predicted
F/60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
Query Match 40.8%; Score 561; DB 1; Length 231;
Best Local Similarity 46.7%; Pred. No. 2.7e-38;

Matches	107;	Conservative	39;	Mismatches	77;	Indels	6;	Gaps	4;
QY	21	KI FNGTECGNNSQPMQVGLFEFTSLRCGGVLIIDHRVLTAAHCGSGRYVRLGHSISQL							80
Db	8	KIVGGYTCFAANASIPVOYSLNNGSHF-CGSGSLINSQMWVASAHACYKSRIQVRLGHNIDVL							66
QY	81	DMTEQIRHSGRSVNHPGVLGASTSHEHDLRLRLPRVNSSVQPLPLPMDCATAGNEC							140
Db	67	EGNEQFINAAKIITHPNFG--NTLDDNDIMLIKSSPFTLSRYATVSLPSCAAAGTEC							124
QY	141	HVSGMGITNHRNPEDLLQCLNLSIVSHATCHGVYGPGRITSNVCAGVH-GQDACQGD							199
Db	125	LISGNGTKSSGSSYPLQCLKAPVLSDSCKSSYFQQTGNMIVGFLGKDS CGD							184
QY	200	SGGRLVCGGVQLGLVSWGSGVPGCGDGLIPGYTYICRVYDMIRIMIRN							248
Db	185	SGGRLVCGGVQLGLVSWG--GCAQKNKPGYTYICRVYDMIRIMIRN							231

RESULT 5
A35871
trypsin (EC 3.4.21.4) precursor, pancreatic - African clawed frog
C|Species: Xenopus laevis (African clawed frog)
C|Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C|Accession: A35871, S12117
R|Shi, Y.B.; Brown, D.D.
Gene Dev. 4, 1107-1113, 1990
A|Title: Developmental and thyroid hormone-dependent regulation of pancreatic genes in X
A|Reference number: A35871, MUID:91007255, PMID:2210372
A|Accession: A35871
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-243 <SH1>
A|Cross-references: UNIPROT:P19799; EMBL:X53458; NID:g65162; PDB:CAA37538.1; PID:g65162
C|Superfamily: trypsin; trypsin homology
C|Keywords: hydrolase; protein digestion; serine proteinase
F|1-15/Domain: signal sequence #status predicted <SIG>
F|16-20/Domain: activation peptide #status predicted <APT>
F|21-236/Domain: trypsin homology <TRY>
F|26-243/Product: trypsin I #status predicted <MT>
F|27-157,45-61,129-230,136-203,168-182/Dissulfide bonds: #status predicted
F|60,104,197/Active site: His, Asp, Ser #status predicted

	Query March Beat Local Similarity 45.7%	Score 555	DB 2	Length 243
	Matches 113	Conservative 42	Mismatches 82	Indels 10
				Gaps 6
Qy	6	FLLLCVGLGSLQAAT--PKIFNGTECGRRNSQPMQVGLFEGETSLRGGVLTIDHRWVLTAAH	62	
Db	3	FLLLCVL-LGAAAAAFDDDKIKIGATCAKSSVPYIYLSNGYHF-CGGSLLTNQWVSAAH	60	
Qy	63	CGSGRWYWRLEAHSLSQLDWTEQIRHSGFSTYHPGLGASTSHEDRLRLRLRPVYTS	122	
Db	61	CYKASIQVRLEHHNIALSEGTQPISSSKYIRHSGY--NSTTLDNDIVLLKSSPASILNA	118	
Qy	123	SVQPLPLENDCAATGTECHVSGWGITNHPNPFDDLIQCLNLSIVSHAATCHGVYGRITS	182	
Db	119	AVNTVPLPSPGCSAAGTSCILISGMGNTLSNGSNYPDLLQCLNAPILITNNAQCSNAPGETTA	178	
Qy	183	NMWCAAGVP-GQDAQQGDSGGPILVCGVLTQGLVSGWGSVPCGGGQIGPVYVYICKYDWI	241	
Db	179	NMICYGVHGGKSDCCQDDSGGPVVCNGQLQGVSNGR--GCAMKNRYGVYTKVCYNAMI	236	
Qy	242	RMIMERN	248	
Db	237	QNTIAAN	243	

RESULT 6
A53968
serine proteinase SCCE precursor - human
N/Alternate names: gastrin corneum chymotryptic enzyme
C/Species: Homo sapiens (man)

C.Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C.Accession: A53968
R.Hanson, L.; Stromqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egeland, T.
J. Biol. Chem. 269, 19420-19426, 1994
A.Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A.Reference number: A53968; MUID:94308225; PMID:8034709
A.Accession: A53968
A.Status: preliminary
A.Molecule type: mRNA
A.Reads: 1-253 <HAN>
A.Cross-references: UNIPROT:P49862; GB:IJ3404; NID:G521214; PIDN:AAC37551.1; PID:G532504
C.Genetics:
A.Gene: GDB:PRSS6; SCCE
A.Cross-references: GDB:377730
A.Map position: 7q35-7q35
C.Superfamily: trypsin; trypsin homology
F:30-245/Domain: trypsin homology <TRY>

Query Match	40.4%	Score 555	DB 2	Length 253
Best Local Similarity	44.6%	Pred. No. 9.2e-38		
Matches	115	Conservative 37	Mismatches 90	Indels 16
			Gaps 6	
QY	1	MGSLFIILLCVGLS-----QAAIPKIFNGTECGRNSQPMOVGLPEGTSILRCGGVLI	52	
DB	1	MRSLLRPLQIILLSLALETAGEEAGCDKIIIDGAPCARSGSPWVALISGNQLHCGGVIV	60	
QY	53	DHRVLTAAHCGSGSRVYVRLGHEHSLQIDWTEQIRHSGFSVTHRGYLGASTSHEHDLRL	112	
DB	61	NERWULTAAHCKKNETVYHLSGDTLG--DRAQRIRKSKSPRHGY--STQTHVNDMLIV	116	
QY	113	RLRLPVRTSSVQPLPLPNDCAATAGTECHVSGWGITNHPNRPFDLLQCLNLSIVSHATC	172	
DB	117	KLNSQARLSISMVYKVALRSPRCBPPTCTVSGWGTTTSPDTPPSDLMCVDPKLSIPQC	176	
QY	173	HGVYPERITSSNMVACAGVPG--QDACGDSGGPLVCGGVTLGLYSWGSVGGPGGDGIPRV	230	
DB	177	TKVYKDLLSNSMLCA-GIPDSKNACNGDSGGPLVCGTGLGLVSWGTF-PCGQPNPDGV	234	
QY	231	VYVICKYVDIMIRIMENN	248	
DB	235	YTVQVCKFTKWMINDTMKKH	252	

RESULT 7
B25528
trypsin (EC 3.4.21.4) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B25528
R:Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A:Title: Sequence organisation and transcriptional regulation of the mouse elastase II a
A:Reference number: A93646; M0ID:87066713; PMID:3641189
A:Accession: B25528
A:Molecule type: mRNA
A:Residues: 1-246 <STE>
A:Cross-references: UNIPROT:P07146; GB:X04574; NID:g54918; PIND:CAA28243.1; PID:g54919
C:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-246/Product: trypsin #status predicted <MAT>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,177,80,95/Binding site: calcium (Glu, Asn, Val, Gln) #status predicted

Query Match	40.2%	Score 553	DB 2	Length 246
Best Local Similarity	44.7%	Pred. NO. 1.3e-37		
Matches 113	Conservative 45	Mismatches 81	Indels 14	Gaps 7

Qy	3	LSIFLLCVLGSQA----	ATPKI	PNGTGECGRNSQPMQVGLFE	EGTSLRCGVLIDHRWL	58
Db	1	MSALLILALVGAAPPPVDDDDK	IVIGSYT	CRESSVPPQVSLNAGH	TF--CGSLINDQWV	59

F/16-23/Domain: activation peptide #status predicted <APT>
F/24-24/Product: trypsin, anionic #status predicted <ENZ>
F/24-23/Domain: trypsin homology <TRY>
F/30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F/63,107,200/Active site: His, Asp, Ser #status predicted
F/75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.7%; Score 546; DB 1; Length 247;
Best Local Similarity 45.6%; Pred. No. 4.8e-37;
Matches 113; Conservative 38; Mismatches 85; Indels 12; Gaps 6;

QY 7 LLLCVLGLSQAATP-----KIFNGTECGRNSQPMQVGLFEGETSLRCGGVLIIDHRWVLLAA 61
Db 5 LILAFGL-AAVATFTDDDDKIVGGTTEGENSVPRQVSLNAGYHF-CGGSLISDQMVVSA 62
QY 62 HCGSGSRVWRIGESLSQDWTETQIRHSGSVTHPGYLGASTSHEDRLRLRLPRVVT 121
Db 63 HCYSKRIOVRLGEVNIIDLENGEQFINSAKVIIRHPNY--NSWIIDNDIMLIKLSPPAVLN 120
QY 122 SSVQPLPLPNDCAATAGTECHVSGWGITNHPNPFPDILQCLNLSIVSHATCHGVYPGBIT 181
Db 121 ARVATISLPRCAAPRGYQCLISGWGNTLSGCTNPELQLCDAPLTQACEASTYPGQIT 180
QY 182 SNNVCAGGV-P-GODACGDSGSPVLCGVLQGLVSWGSGVPCGQDGLPGVYTYICKYVDM 240
Db 181 ENMTCAGLEGGKXSCGDSGSPVVCNCELQIGVSMGY--GCAQKRGKGYTTKVCNPFVDM 238
QY 241 IRMIRMNN 248
Db 239 IQSTIAAN 246

RESULT 11

TRDC
trypsin (EC 3.4.21.4) precursor, cationic - dog
N/Alternate names: cationic trypsinogen
C/Species: Canis lupus familiaris (dog)
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C/Accession: B26273
R/PinkB, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A/Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequence
A/Reference number: A26273; MUID:86284628; PMID:3841794
A/Accession: B26273
A/Molecule type: mRNA
A/Residues: 1-246 <PIN>
A/Cross-references: UNIPROT:P06871; GB:M11590; NID:G164096; PIDN:AAA30900.1; PID:G164097
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F/1-15/Domain: signal sequence #status predicted <SIG>
F/16-23/Domain: activation peptide #status predicted <APT>
F/24-24/Product: trypsin, cationic #status predicted <ENZ>
F/24-23/Domain: trypsin homology <TRY>
F/30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F/63,107,200/Active site: His, Asp, Ser #status predicted
F/75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.7%; Score 545; DB 1; Length 246;
Best Local Similarity 44.2%; Pred. No. 5.8e-37;
Matches 111; Conservative 43; Mismatches 87; Indels 10; Gaps 6;

QY 3 LSLFLLCVLGLSQA-----ATPKIFNGTECGRNSQPMQVGLFEGETSLRCGGVLIIDHRVYL 58
Db 1 MKTIFLALGATVAFPIDDDDKIVGGTTCGRNSVPVQVSLNSGHR-CGGSLISQMVV 59
QY 59 TAAACGSGRVWRIGESLSQDWTETQIRHSGSVTHPGYLGASTSHEDRLRLRLPRV 118
Db 60 SAACHVSRIVRGVNIIVASEEGEGFINAKIIRHRY-NANTYI-DNDIMLIKLSPPA 117
QY 119 RVTSVQPLPLPNDCAATAGTECHVSGWGITNHPNPFPDILQCLNLSIVSHATCHGVYPG 178
Db 118 TLNRSVSAIALPKSCPAAGTQCLISGWGNTSIGQVNDVLIQCKAPILSDSVCRNAPFG 177

QY 179 RITSNNVCAGGV-P-GODACGDSGSPVLCGVLQGLVSWGSGVPCGQDGLPGVYTYICKY 237
Db 178 QISSNNMCLGMEGGKXSCGDSGSPVVCNCELQIGVSMGY--GCAQKRGKGVPRVKCY 235
QY 238 VDMIRMNN 248
Db 236 VSWIQSTIAAN 246

RESULT 12

A27547
trypsin (EC 3.4.21.4) precursor, cationic - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: A27547
R/Fletcher, T.S.; Alnadeff, M.; Craik, C.S.; Largman, C.
Biochemistry 26, 3081-3086, 1987
A/Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen.
A/Reference number: A27547; MUID:87271609; PMID:3607011
A/Accession: A27547
A/Molecule type: mRNA
A/Residues: 1-247 <FILE>
A/Cross-references: UNIPROT:P08426; GB:M16624; NID:G206498; PIDN:AAA1985.1; PID:G206499
C/Superfamily: trypsin; trypsin homology
C/Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F/25-240/Domain: trypsin homology <TRY>
F/31-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
F/64,108,201/Active site: His, Asp, Ser #status predicted
F/76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.6%; Score 544.5; DB 2; Length 247;
Best Local Similarity 43.3%; Pred. No. 6.3e-37;
Matches 109; Conservative 43; Mismatches 89; Indels 11; Gaps 5;

QY 3 LSLFLLCVLGLSQA-----TPKIFNGTECGRNSQPMQVGLFEGETSLRCGGVLIIDHRV 57
Db 1 MKALIFLAFGLAAVALPLDDDDKIVGGYTQCKNSLPYQVSLNAGYHF-CGGSLINSQMV 59
QY 58 LTAACGSGRVWRIGESLSQDWTETQIRHSGSVTHPGYLGASTSHEDRLRLRLP 117
Db 60 VSAACHCKSRQVRLGEHNIIDVGGQFIDAAKIIRHPY--NANTFNDIMLIKLSNP 117
QY 118 VRVTSVQPLPLPNDCAATAGTECHVSGWGITNHPNPFPDILQCLNLSIVSHATCHGVY 177
Db 118 ATLNSRVSTVSLPSCSSSGTKLVSGWNTLSGCTNPELQLCDAPLVSDSSCKSYR 177
QY 178 GRITSNNVCAGGV-P-GODACGDSGSPVLCGVLQGLVSWGSGVPCGQDGLPGVYTYICK 236
Db 178 GKITSNNFCLGFLGKXSCGDSGSPVVCNCELQIGVSMGY--GCAQKRGKGYTTKVCN 235
QY 237 YVDMIRMNN 248
Db 236 YVNMIIQSTIAAN 247

RESULT 13

TRRTI
trypsin (EC 3.4.21.4) I precursor - rat
N/Alternate names: trypsinogen I
C/Species: Rattus norvegicus (Norway rat)
C/Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C/Accession: B22657; A00948
R/Craig, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A/Title: Structure of two related rat pancreatic trypsin genes.
A/Reference number: A22657; MUID:85054880; PMID:6094547
A/Accession: B22657
A/Molecule type: DNA
A/Residues: 1-246 <CRA>
A/Cross-references: UNIPROT:P00762; GB:J00778; NID:G206507; PIDN:AAA98518.1; PID:G206508
A/Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17.
R/MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982

A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of
A;Reference number: A00948; MUID:82265624; PMID:6696710
A;Accession: A00948
A;Molecule type: mRNA
A;Residues: 1-246 <MOL>
A;Cross-references: GB:000778; NID:g206507; PIDN:AAA98518.1; PID:g206508
C;Genetics:
A;Intons: 14/1; 67/2; 152/1; 197/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-23/Domain: activation peptide #status predicted <APR>
F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.5%; Score 543; DB 1; Length 246;
Best Local Similarity 44.5%; Pred. No. 8,4e-37;
Matches 110; Conservative 47; Mismatches 76; Indels 14; Gaps 7;

QY 3 LSTIFLLCYLGSQA---ATPKIFNGTCGRNSQPMOYGLFEGTSLRCGVLIDHRVYL 58
DB 1 MSHLLTALAIVGAANAPLPEDDDKIVGGYTCPEHSVPYQVSLNSGYHF-CGGSLINDQWV 59
QY 59 TAAHCGSRVWYRLGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEDRLRLRLPV 118
DB 60 SAHCKYKRIQVRLGHNINIVLEGEQFINKAKIKHRY--SSMTLNDNDIMLITLSPV 117
QY 119 RYTSVQPLPLPNDCAVTAGTECHVSGWG--ITNFRNPEDLLQCLNLSIVSHATCGVY 176
DB 118 KLNARAPALPALSACAPATQCLISGNGVTLNSGVN--PDLLQCVDAPIVLSQDCEANAY 175
QY 177 PGRITSNWYACAGVP-GODACQDGGPVLGGLVSGVSGVPCGQDGIPIGVYTYIC 235
DB 176 PGRITSNWYACAGVP-GODACQDGGPVLGGLVSGVSGVPCGQDGIPIGVYTYIC 235
QY 236 KYVDMIR 242
DB 234 NFVGMIQ 240

RESULT 14
S31779
trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S66657; S31779
R;Male, R.; Lorenz, J.B.; Smalae, A.O.; Torrisen, K.R.
Burr, J. Biochem. 232, 677-685, 1995
A;Title: Molecular cloning and characterization of anionic and cationic variants of try
A;Reference number: S66657; MUID:96035908; PMID:7556223
A;Accession: S66657
A;Molecule type: mRNA
A;Residues: 1-238 <MAL>
A;Cross-references: UNIPROT:P35033; EMBL:X70074; NID:964387; PIDN:CAA9679.1; PID:964388
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F;8-15/Domain: activation peptide #status predicted <APT>
F;16-238/Product: trypsin III #status predicted <MAT>
F;16-231/Domain: trypsin homology <TRY>
F;22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted
F;55,99,192/Active site: His, Asp, Ser #status predicted

Query Match 39.3%; Score 540; DB 2; Length 238;
Best Local Similarity 47.2%; Pred. No. 1,4e-36;
Matches 108; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

QY 21 KIFNGTCGRNSQPMOYGLFEGTSLRCGVLIDHRVLTAAHCGSRVWYRLGHSLSQ 80
DB 15 KIVGGEHCRNSASYSQSLSGYHF-CGGSLISTWVNSAHCYKSRIVRLGHNIAVNV 73

QY 81 DWTEQIRHSGFVTHPGYLGASTSHEDRLRLRLPVRYTSVQPLPLPNDCAVTAGTEC 140
DB 74 EGTEQFIDSVKVIWHPST--NSRMLDNDIMLIKLSKPAASLNSYSTVALSSCASSCTTC 131
QY 141 HVSQMGITNHRNRPEDLLQCLNLSIVSHATCGVYGRITTSNWCAGVP-GODACQD 199
DB 132 LVSGMGLNSGSSSNYPPTLRCLDPLISSSCNSAYGQITSNMFCAGFMEGKDCQGD 191
QY 200 SGGPVLGCVGLQGLVSGVSGVPCGQDGIPIGVYTYICKYVMIMIRNN 248
DB 192 SGGPVLGCVGLQGLVSGVSGVPCGQDGIPIGVYTYICKYVMIMIRNN 238

RESULT 15
S05494
trypsin (EC 3.4.21.4) IV precursor - rat
N;Alternate names: 23K protein; trypsinogen IV precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S05494
R;Luetteke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.
Nucleic Acids Res. 17, 6736, 1989
A;Title: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.
A;Reference number: S05494; MUID:89386010; PMID:2780302
A;Accession: S05494
A;Molecule type: mRNA
A;Residues: 1-247 <LUE>
A;Cross-references: UNIPROT:P12788; EMBL:X15679; NID:g56813; PIDN:CAA33718.1; PID:g56814
C;Superfamily: trypsin; trypsin homology
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-23/Domain: activation peptide #status predicted <APR>
F;24-247/Product: trypsin IV #status predicted <MAT>
F;24-240/Domain: trypsin homology <TRY>
F;30-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 38.8%; Score 533.5; DB 2; Length 247;
Best Local Similarity 43.4%; Pred. No. 4,9e-36;
Matches 109; Conservative 41; Mismatches 94; Indels 7; Gaps 4;

QY 1 MGSIF--LILCYLGSQAATPKIFNGTCGRNSQPMOYGLFEGTSLRCGVLIDHRVYL 58
DB 1 MKSIFAFPLGAANALPVDDDDKIVGGYTCPEHLPYQVSLHDSHQCGSLIDQWV 60
QY 59 TAAHCGSRVWYRLGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEDRLRLRLPV 118
DB 61 SAHCKYKRIQVRLGHNINIVLEGEQFINKAKIRHPEY--NKDTLNDNDIMLIKSPA 118
QY 119 RYTSVQPLPLPNDCAVTAGTECHVSGWGITNHRNPEDLLQCLNLSIVSHATCGVY 178
DB 119 VANSQVSTVSLRSCASDAQCLVSGKNTVSGKTYPALQCAPVLSASSCKKSPG 178
QY 179 RYTSNWCAGVP-GODACQDGGPVLGGLVSGVSGVPCGQDGIPIGVYTYICKY 237
DB 179 QITSNMFCGLFEGKDCDSDGSPVVCNBEIQIVSGV--CANMGRKGVTTKVCNY 236
QY 238 VDMIMIRNN 248
DB 237 LSWIETMANN 247

Search completed: March 5, 2005, 18:17:26
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 5, 2005, 18:13:09 ; Search time 176 Seconds

(without alignments)
721.566 Million cell updates/sec

Title: US-10-006-116A-194

Perfect score: 1374

Sequence: 1 MGSLIFLLCLVGLSQAAP.....GVYTYCKYVDIMIMRNN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1374	100.0	248	1	KLK6_HUMAN
2	952.5	69.3	234	2	O9CV76
3	630.5	45.9	260	1	KLK8_HUMAN
4	627.5	45.7	260	2	O81W69
5	622.5	45.3	260	1	NRPN_MOUSE
6	621.5	45.2	260	1	NRPN_MOUSE
7	618.5	45.0	250	1	KLK8_HUMAN
8	611	44.5	255	2	O7JIG6
9	610	44.4	250	2	O63ZP2
10	608	44.3	254	2	O8CGR4
11	601	43.7	255	2	O81XD7
12	599	43.6	275	2	O6IS10
13	599	43.6	256	1	KLK6_HUMAN
14	597.5	43.5	249	2	O9QVY4
15	597.5	43.5	276	2	O9QYV3
16	595	43.3	255	2	O96R00
17	588.5	42.8	293	2	O9D140
18	588	42.6	276	2	O8CGR6
19	586	42.6	250	2	O8CGR5
20	578	42.1	242	2	O80V54
21	576	41.9	246	2	O6P3Z0
22	569.5	41.4	248	1	TRY3_CHICK
23	569.5	41.4	251	1	KLKE_HUMAN
24	569.5	41.4	251	2	O6B089
25	568.5	41.4	250	1	KLK9_HUMAN
26	567	41.3	277	1	KLKD_HUMAN
27	566	41.2	248	1	TRY2_CHICK
28	565	41.1	248	1	TRY1_CHICK
29	564.5	41.0	293	1	KLK5_HUMAN
30	564	41.0	276	1	KLK4_HUMAN
31	563	41.0	244	1	TRY2_XENLA

32	563	41.0	248	2	O7SZT1
33	562	40.9	255	2	O6GMU2
34	561	40.8	231	1	TRY6_PIG
35	561	40.8	243	1	TRY1_BOVIN
36	561	40.8	243	1	KLK6_HUMAN
37	557	40.5	237	2	O6GY05
38	555	40.4	243	1	TRY1_XENLA
39	555	40.4	243	2	O7SZ06
40	555	40.4	253	1	KLK7_HUMAN
41	553.5	40.3	246	2	O88301
42	553.5	40.3	253	2	O91Y82
43	553	40.2	246	1	TRY2_MOUSE
44	550.5	40.1	247	2	O9D7Y7
45	550	40.0	247	1	TRY2_BOVIN
46	549.5	40.0	247	2	O9CPN9
47	548	39.9	246	2	O6IE66
48	546.5	39.8	251	2	O54854
49	546	39.7	247	1	TRY2_CANPA
50	545	39.7	246	1	TRY1_CANPA
51	544.5	39.6	247	1	TRY3_RAT
52	544	39.6	253	2	O8N5N9
53	543	39.5	246	1	TRY1_RAT
54	543	39.5	246	2	O792Z1
55	541.5	39.4	247	2	O9CPN7
56	541.5	39.4	238	1	TRY3_SALSA
57	540	39.3	246	2	O792Y8
58	538.5	39.2	249	2	O91VE3
59	536	39.0	246	2	O7TT42
60	536	39.0	246	2	O9R0T7
61	535.5	39.0	245	2	O6R670
62	535.5	39.0	261	2	O6H320
63	534.5	38.9	245	2	O6R671
64	533.5	38.8	245	2	O792Y9
65	533.5	38.8	247	1	TRY4_RAT
66	533	38.8	246	1	TRY2_RAT
67	533	38.8	246	2	O921R9
68	532	38.7	246	2	O9QUK9
69	528	38.4	246	2	O792Z0
70	528	38.4	263	2	O6H319
71	527.5	38.4	261	1	KLK7_RAT
72	525	38.2	240	2	O98T54
73	523.5	38.1	246	2	O7M754
74	522	38.0	244	2	O8QGW3
75	521.5	38.0	246	1	KLK6_MOUSE
76	521.5	38.0	261	1	KLK6_MOUSE
77	520.5	37.9	256	2	O63ZF4
78	519	37.8	246	1	TRYA_RAT
79	518	37.7	246	1	TRYB_RAT
80	518	37.7	261	1	KLK8_RAT
81	514.5	37.4	242	2	O7T1R8
82	514	37.4	239	2	O63Z75
83	513.5	37.4	231	1	TRY2_SALSA
84	513.5	37.4	243	1	KLK2_CAVPO
85	513.5	37.4	243	2	O8AV83
86	513.5	37.4	261	2	O9N1Q1
87	513.5	37.4	278	2	O99M20
88	512	37.3	279	2	O6IE55
89	511.5	37.2	261	2	O93474
90	510.5	37.2	238	2	O9W706
91	510.5	37.2	261	1	KLK3_MOUSE
92	509.5	37.1	222	2	O8AV11
93	509.5	37.1	235	2	O63Z74
94	508	37.0	242	1	TRY1_SALSA
95	508	37.0	242	2	O9W7Q7
96	507	36.9	244	2	O42159
97	507	36.9	259	2	O63ZP5
98	506	36.8	245	2	O42160
99	505	36.8	242	2	O7SX90
100	505	36.8	249	2	O92046
101	505	36.8	260	1	EST1_CANPA
102	505	36.8	282	2	O76B45
103	504.5	36.7	269	2	O8IU55
104	503	36.6	241	2	O98TQ9

O7sz1	xenopus lae
O6gm2	xenopus lae
P00761	sus scrofa
P00760	bos taurus
O92876	homo sapien
O6gy15	strehlo ca
P19799	xenopus lae
O7sz06	xenopus lae
P49862	homo sapien
O88301	mus muscu
O91y82	mus muscu
P07146	mus muscu
O9d7y7	mus muscu
O29463	bos taurus
O9cpn9	m mus muscu
O6ie66	rattus norv
O54854	rattus norv
P06872	canis faml
P06871	canis faml
P08426	rattus norv
O8n5n9	homo sapien
P00762	rattus norv
O792z1	mus muscu
O9cpn7	mus muscu
P35033	salmo salar
O792y8	mus muscu
O91ve3	m thymopai
O7tc42	mus muscu
O910c7	m pancreat
O6r670	oreochromis
O6h320	bos taurus
O6r671	oreochromis
O792y9	mus muscu
P12788	rattus norv
P00763	rattus norv
O921r9	mus muscu
O9quk9	mus muscu
O792z0	mus muscu
O6h319	sus scrofa
P36373	rattus norv
O98t54	engraulis j
O7m754	mus muscu
O8qgw3	anguilla ja
P00752	sus scrofa
P15947	mus muscu
O63zf4	rattus norv
P32821	rattus norv
P32822	rattus norv
P36374	rattus norv
O711r8	pangasius h
O63z75	rattus norv
P35032	salmo baler
P12323	cavia porce
O8av83	brachydanio
O9n1q1	saginus oe
O99m20	mus muscu
O6ie55	rattus norv
O93474	canis faml
O9w706	paralichthy
P00716	mus muscu
O8av11	oncorhynch
O63z74	rattus norv
P35031	salmo salar
O9w7q7	paralichthy
O42159	petromyzon
O63zpf5	rattus norv
O42160	petromyzon
O7sx90	brachydanio
O92046	disoetichu
P05582	canis faml
O76b45	blarina bre
O8iu55	homo sapien
O98tq9	engraulis j

105	503	36.6	263	1	KLKR PRANA	P32824	praomys nat	178	458.5	33.4	261	1	KLK2 HUMAN	P20151	homo sapien
106	502	36.5	249	2	Q9W6FO	Q9W6FO	notothenia	179	452	32.9	260	1	Q710F4	Q710F4	trimeresuru
107	502	36.5	259	1	KLKC RAT	P36376	rattus norv	180	451	33.8	260	2	Q7T229	Q7T229	bothrops ja
108	501.5	36.5	237	2	Q91515	Q91515	fugu rubrip	181	450	33.8	260	2	Q8UYX1	Q8UYX1	agkistrodon
109	501	36.5	242	2	Q93266	P07478	pseudopleur	182	449	32.7	258	1	VSP1 TRIST	Q91516	trimeresuru
110	501	36.5	247	1	TRX2 HUMAN	P07478	homo sapien	183	448	32.7	258	2	Q8AY78	Q8AY78	trimeresuru
111	501	36.5	247	2	Q9W705	Q91041	paralichthy	184	446.5	32.5	257	2	Q710I5	Q710I5	trimeresuru
112	499.5	36.4	241	1	TRIX GADMO	Q91041	gadus morhu	185	445.5	32.4	249	2	VSP3 TRIMU	Q91509	trimeresuru
113	499	36.3	239	2	Q8N1C9	Q91041	gadus morhu	186	444.5	32.4	257	2	VSP3 TRIMU	Q91509	trimeresuru
114	498	36.2	249	2	Q788V0	Q91041	gadus morhu	187	443	32.2	258	1	VSP2 AGKAC	Q81F47	gadus morhu
115	498	36.2	254	1	KLK4 HUMAN	Q91041	gadus morhu	188	443	32.2	258	1	VSP3 BORJA	Q91509	trimeresuru
116	497	36.2	254	1	KLK4 HUMAN	Q91041	gadus morhu	189	439.5	32.0	257	2	VSP7 TRIMU	Q81F47	gadus morhu
117	497	36.2	257	2	Q61B61	Q91041	gadus morhu	190	439	32.0	257	2	VSP7 TRIMU	Q81F47	gadus morhu
118	497	36.2	261	2	Q725F4	Q91041	gadus morhu	191	438	31.9	259	2	Q9YGJ8	Q91509	trimeresuru
119	496.5	36.1	261	2	KLK1 PAPHA	Q91041	gadus morhu	192	437.5	31.8	257	1	VSP2 TRIMU	Q91509	trimeresuru
120	496	36.1	242	2	KLK3 MOUSE	Q91041	gadus morhu	193	437.5	31.8	257	1	VSP4 TRIMU	Q91509	trimeresuru
121	496	36.1	242	2	Q92059	Q91041	gadus morhu	194	436.5	31.8	257	2	Q9PT51	Q91509	trimeresuru
122	496	36.1	247	2	Q42158	Q91041	gadus morhu	195	436.5	31.8	257	2	Q9PT51	Q91509	trimeresuru
123	496	36.1	247	2	Q42608	Q91041	gadus morhu	196	436.5	31.8	257	1	VSP1 TRIMU	Q91509	trimeresuru
124	495.5	36.1	257	1	Q86061	Q91041	gadus morhu	197	435.5	31.8	257	1	VSP5 TRIMU	Q91509	trimeresuru
125	495.5	36.1	257	1	KLK3 MACFA	Q91041	gadus morhu	198	435.5	31.8	257	1	VSP5 TRIMU	Q91509	trimeresuru
126	495	36.0	261	2	Q725F3	Q91041	gadus morhu	199	435	31.7	258	1	VSP2 TRIJE	Q91509	trimeresuru
127	495	36.0	261	2	Q6H322	Q91041	gadus morhu	200	434	31.6	258	1	VSP3 TRIJE	Q91509	trimeresuru
128	494.5	35.9	247	1	TRX1 HUMAN	Q91041	gadus morhu	201	434	31.6	258	1	VSP3 TRIJE	Q91509	trimeresuru
129	493.5	35.9	248	2	Q66105	Q91041	gadus morhu	202	434	31.6	258	1	VSP3 TRIJE	Q91509	trimeresuru
130	493	35.9	262	2	KLK1 HUMAN	Q91041	gadus morhu	203	433.5	31.6	257	2	Q710I9	Q91509	trimeresuru
131	492	35.8	262	2	Q66U59	Q91041	gadus morhu	204	433	31.5	257	2	VSP1 AGKHP	Q91509	trimeresuru
132	491.5	35.8	262	2	TRX1 GADMO	Q91041	gadus morhu	205	433	31.5	257	2	VSP1 AGKHP	Q91509	trimeresuru
133	491	35.7	256	1	KLK4 MOUSE	Q91041	gadus morhu	206	432	31.4	257	2	VSP2 DABRU	Q91509	trimeresuru
134	490.5	35.7	229	1	TRYP SQUAC	Q91041	gadus morhu	207	432	31.4	257	2	Q9PTL3	Q91509	trimeresuru
135	490.5	35.7	261	1	KLK2 MOUSE	Q91041	gadus morhu	208	432	31.4	257	2	VSP2 AGKHP	Q91509	trimeresuru
136	489.5	35.6	261	1	KLK2 MOUSE	Q91041	gadus morhu	209	431.5	31.4	257	2	Q710B0	Q91509	trimeresuru
137	489	35.6	244	2	KLK4 RAT	Q91041	gadus morhu	210	431.5	31.4	257	2	Q96JEO	Q91509	trimeresuru
138	488	35.5	247	2	Q8NHM4	Q91041	gadus morhu	211	431.5	31.4	257	2	Q710B1	Q91509	trimeresuru
139	487.5	35.5	251	2	Q9DBO8	Q91041	gadus morhu	212	431.5	31.4	257	1	KLK2 HORSE	Q91509	trimeresuru
140	486	35.4	242	2	Q6R179	Q91041	gadus morhu	213	431	31.4	260	1	KLK2 MOUSE	Q91509	trimeresuru
141	485.5	35.3	234	2	Q9R048	Q91041	gadus morhu	214	431	31.4	260	1	VSPA TRIGA	Q91509	trimeresuru
142	485.5	35.3	261	2	Q88309	Q91041	gadus morhu	215	429.5	31.3	262	1	VSP1 AGKCA	Q91509	trimeresuru
143	484.5	35.3	251	2	Q8N2U3	Q91041	gadus morhu	216	429	31.2	262	2	Q96JEO	Q91509	trimeresuru
144	484.5	35.3	259	1	KLK2 MOUSE	Q91041	gadus morhu	217	429	31.2	262	2	Q8KSD7	Q91509	trimeresuru
145	484.5	35.3	304	1	TRX3 HUMAN	Q91041	gadus morhu	218	429	31.2	262	2	VSP3 TRIGA	Q91509	trimeresuru
146	484	35.2	255	2	Q9ZOM1	Q91041	gadus morhu	219	429	31.2	262	2	Q8OHK3	Q91509	trimeresuru
147	483.5	35.2	261	1	KLK1 RAT	Q91041	gadus morhu	220	428.5	31.2	262	2	Q8OHK3	Q91509	trimeresuru
148	483.5	35.2	265	2	Q68G17	Q91041	gadus morhu	221	427	31.1	260	2	Q93502	Q91509	trimeresuru
149	482	35.1	255	2	Q691S2	Q91041	gadus morhu	222	426.5	31.0	257	1	VSPC TRIGA	Q91509	trimeresuru
150	481.5	35.0	261	1	KLK3 MOUSE	Q91041	gadus morhu	223	425	30.9	260	1	VSP1 AGKAC	Q91509	trimeresuru
151	481	35.0	261	1	KLK3 MOUSE	Q91041	gadus morhu	224	424.5	30.9	257	2	VSP1 AGKAC	Q91509	trimeresuru
152	480.5	35.0	254	2	Q9XSN6	Q91041	gadus morhu	225	424.5	30.9	257	2	VSP1 AGKCA	Q91509	trimeresuru
153	479	34.9	261	1	KLK3 MOUSE	Q91041	gadus morhu	226	423	30.8	260	2	VSP1 AGKCA	Q91509	trimeresuru
154	479	34.9	261	1	KLK3 MACMU	Q91041	gadus morhu	227	422.5	30.7	259	2	Q8UYX1	Q91509	trimeresuru
155	478.5	34.8	248	2	Q6DT45	Q91041	gadus morhu	228	422.5	30.7	259	2	Q8UYX1	Q91509	trimeresuru
156	478.5	34.8	250	2	Q93265	Q91041	gadus morhu	229	421.5	30.7	256	2	Q8UYX1	Q91509	trimeresuru
157	477.5	34.8	256	2	Q61E12	Q91041	gadus morhu	230	421.5	30.7	256	2	Q8UYX1	Q91509	trimeresuru
158	477.5	34.8	261	1	KLK1 MOUSE	Q91041	gadus morhu	231	420.5	30.6	257	2	Q6EH01	Q91509	trimeresuru
159	477.5	34.8	263	1	KLK1 MOUSE	Q91041	gadus morhu	232	419.5	30.5	257	2	Q710I8	Q91509	trimeresuru
160	477	34.7	247	2	Q66P69	Q91041	gadus morhu	233	419.5	30.5	257	2	Q710I8	Q91509	trimeresuru
161	476.5	34.7	344	2	Q9W6T9	Q91041	gadus morhu	234	418.5	30.5	257	2	Q710I8	Q91509	trimeresuru
162	476.5	34.7	675	2	Q9W6T8	Q91041	gadus morhu	235	418.5	30.5	257	2	Q710I8	Q91509	trimeresuru
163	475.5	34.6	219	2	Q91036	Q91041	gadus morhu	236	417	30.3	236	1	VSPG DABRU	Q91509	trimeresuru
164	472.5	34.6	235	2	Q66P68	Q91041	gadus morhu	237	415.5	30.2	257	2	Q93594	Q91509	trimeresuru
165	471	34.3	249	2	Q66P68	Q91041	gadus morhu	238	415.5	30.2	257	2	Q93594	Q91509	trimeresuru
166	470.5	34.2	257	2	Q66P68	Q91041	gadus morhu	239	414	30.1	257	2	Q93594	Q91509	trimeresuru
167	470.5	34.2	261	1	KLK3 HUMAN	Q91041	gadus morhu	240	413	30.1	258	1	VSP1 TRIGA	Q91509	trimeresuru
168	470	34.2	258	2	Q710I1	Q91041	gadus morhu	241	413	30.1	258	1	VSP1 TRIGA	Q91509	trimeresuru
169	469.5	34.2	261	1	KLK3 MOUSE	Q91041	gadus morhu	242	411.5	29.9	228	1	VSPA LACMU	Q91509	trimeresuru
170	469.5	34.2	261	1	KLK3 MOUSE	Q91041	gadus morhu	243	411.5	29.9	228	1	VSPA LACMU	Q91509	trimeresuru
171	468	34.1	259	1	KLK2 RAT	Q91041	gadus morhu	244	411	29.9	228	1	VSPA LACMU	Q91509	trimeresuru
172	467.5	34.0	261	1	KLK2 RAT	Q91041	gadus morhu	245	411	29.9	228	1	VSPA LACMU	Q91509	trimeresuru
173	467	34.0	258	2	Q710H6	Q91041	gadus morhu	246	411	29.9	228	1	VSPA LACMU	Q91509	trimeresuru
174	462.5	33.7	261	2	Q8K0C6	Q91041	gadus morhu	247	409	29.8	260	2	VSP2 VIPIE	Q91509	trimeresuru
175	461.5	33.6	259	2	KLK3 RAT	Q91041	gadus morhu	248	408.5	29.7	257	2	Q8UH62	Q91509	trimeresuru
176	461	33.6	258	2	Q8AY80	Q91041	gadus morhu	249	408	29.7	235	1	VSP2 AGKBI	Q91509	trimeresuru
177	458.5	33.4	250	1	TRYP_PUEPL	P35034	pleuronecte	250	407	29.6	237	2	Q934Z1	Q91509	trimeresuru

251	407	29.6	258	1	VSP2_AGRCA	042207 agkistrodon	324	361.5	26.3	267	2	Q7S251	Q7e251 brachydanio
252	407	29.6	258	2	08AV79	08av79 trimereuru	325	361	26.3	257	2	06MGR1	06mgr1 itealurus p
253	407	29.6	260	1	VSP2_TRIFL	013057 agkistrodon	326	361	26.3	257	2	0640E1	0640e1 xenopus lae
254	406.5	29.6	231	1	VSP1_AGRCA	Q19872 agkistrodon	327	359.5	26.2	259	2	06AACC2	06aaz2 brachydanio
255	406.5	29.6	257	2	Q11QI5	Q11q13 trimereuru	328	359.5	26.2	259	2	06ISU5	06isus homo sapien
256	405.5	29.5	257	2	Q11QI3	Q11q13 trimereuru	329	359.5	26.2	277	1	TRV2_ANGA	P35036 anopheles g
257	405	29.5	234	2	Q7SZB2	Q7e251 agkistrodon	330	359.5	26.2	342	1	PS88_MOUSE	Q9ea21 mus musculu
258	403.5	29.4	232	2	06IWF1	06iwf1 bothrops al	331	359	26.1	265	2	06P326	06p326 xenopus tro
259	402.5	29.3	232	1	VSP1_BOTUA	P81824 bothrops ja	332	359	26.1	311	2	080XZ3	080xz3 rattus norv
260	402.5	29.3	257	2	Q9YGO9	Q9y939 agkistrodon	333	359	26.1	430	2	0804X0	Q804x0 fugu rubrip
261	402	29.3	255	1	VSPA_BOTAT	P4971 bothrops at	334	358.5	26.1	245	1	MCT1_SHEEP	P80931 ovis aries
262	402	29.3	260	1	VSP1_TRIJU	Q6df68 trimereuru	335	358.5	26.1	444	1	FAT7_RABIT	P88139 oryctolagus
263	402	29.3	260	1	VSP6_TRIJU	Q9d8w9 trimereuru	336	358	26.1	812	1	PLMN_BOVIN	P6868 bos taurus
264	400	29.1	234	1	VSP2_AGRCA	P82991 agkistrodon	337	357.5	26.0	232	2	09XY45	Q9xy45 ctenocephal
265	400	29.1	258	2	0802F0	Q802f0 agkistrodon	338	357.5	26.0	371	2	08MS52	08ms52 drosophila
266	399.5	29.1	257	2	08QGB6	Q8qgb6 bothrops in	339	357.5	26.0	643	2	097506	Q97506 sus scrofa
267	399	29.0	260	2	Q71QJ2	Q71qj2 trimereuru	340	357	26.0	262	1	GRAA_HUMAN	P12544 homo sapien
268	397	28.9	235	2	Q90Z47	Q90z47 agkistrodon	341	357	26.0	263	1	CTRB_HUMAN	P17538 homo sapien
269	397	28.9	260	2	Q71QI4	Q71q14 trimereuru	342	357	26.0	271	1	CTRL_PENVA	Q00871 peneaus van
270	395.5	28.8	264	2	Q9ER05	Q9er05 mus musculu	343	357	26.0	806	1	PLMN_MACEU	Q18763 macroptus eu
271	395	28.7	260	2	Q71QI9	Q71q19 trimereuru	344	357	26.0	1019	1	LFC_FACR	P28175 tachypneus
272	394.5	28.7	257	1	VSP2_BOTUA	Q13068 bothrops ja	345	357	26.0	1019	2	0819S1	Q819s1 tachypneus
273	393.5	28.6	264	2	Q9D7P8	Q9d7p8 mus musculu	346	356.5	25.9	261	2	Q9W7Q4	Q9w7q4 lepeophthei
274	393	28.6	260	1	VSPA_AGRAC	Q918w9 agkistrodon	347	356.5	25.9	321	1	TRYG_HUMAN	Q9ur12 homo sapien
275	392	28.5	258	2	Q71QI2	Q71q12 trimereuru	348	356.5	25.9	321	2	Q96RZ8	Q96rz8 homo sapien
276	391.5	28.5	264	2	Q9EQZ8	Q9eqz8 rattus norv	349	355.5	25.9	260	2	Q9V7G4	Q9v7g4 drosophila
277	391	28.5	253	2	08WZB4	Q8wzb4 homo sapien	350	355.5	25.9	276	1	MCT6_MOUSE	P19845 mus musculu
278	389	28.3	253	1	CPAD_HUMAN	P00746 homo sapien	351	355	25.8	342	1	PS88_RAT	Q9e87 rattus norv
279	389	28.3	258	2	Q8JH85	Q8jhb5 viperia lebe	352	354.5	25.8	249	2	Q6QX59	Q6qx59 lepeophthei
280	388.5	28.3	257	1	VSP3_TRIFL	Q13058 trimereuru	353	354.5	25.8	311	2	08WZM5	Q8wzm5 trichoderma
281	388	28.2	269	1	EL2_BIG	P08419 sus scrofa	354	354.5	25.8	331	2	Q8R1A6	Q8r1a6 mus musculu
282	387	28.2	181	2	08NFV7	Q8nfv7 homo sapien	355	354.5	25.8	331	2	Q80X17	Q80x17 mus musculu
283	387	28.2	243	2	08EUV5	Q8evu5 homo sapien	356	354	25.8	260	2	Q9W7P9	Q9w7p9 paratichthy
284	387	28.2	258	2	Q98TV5	Q98tv5 agkistrodon	357	354	25.8	271	1	EL2_MOUSE	P95208 mus musculu
285	386.5	28.1	257	1	VSP3_AGRAC	Q918x0 agkistrodon	358	353.5	25.7	263	1	CTRA_GADMO	P47736 gadus morhu
286	386	28.1	232	1	VSPA_BOTUA	P81661 bothrops ja	359	353.5	25.7	270	1	TRYT_MERUN	P50342 meriones g
287	386	28.1	258	2	Q91961	Q91961 agkistrodon	360	353.5	25.7	333	2	Q7Q5Z6	Q7q5z6 anopheles g
288	386	28.1	258	2	Q9W7S1	Q9w7s1 agkistrodon	361	353	25.7	274	1	MCT6_RAT	P50343 meriones g
289	386	28.1	260	2	Q6T6S7	Q6t6s7 agkistrodon	362	353	25.7	314	1	TEST_HUMAN	Q9v6n0 homo sapien
290	385.5	28.1	188	1	KLK3_RAT	P15950 rattus norv	363	353	25.7	456	1	PRTC_HUMAN	Q28278 canis famli
291	385.5	28.1	264	1	CTRL_HUMAN	P40313 homo sapien	364	353	25.7	459	1	PRTC_PIG	Q9g1p2 sus scrofa
292	385.5	28.1	264	2	Q9D960	Q9d960 mus musculu	365	352.5	25.7	263	2	Q6PG84	Q6pg84 xenopus lae
293	385.5	28.0	169	2	Q8IUW0	Q8iuw0 homo sapien	366	352.5	25.7	321	2	Q6GNK3	Q6gnk3 xenopus lae
294	384.5	28.0	195	2	Q07277	Q07277 homo sapien	367	352	25.6	111	2	Q9UKR2	Q9ukr2 homo sapien
295	382.5	27.8	1524	2	Q91674	Q91674 xenopus lae	368	352	25.6	260	1	GRAA_MOUSE	P11032 mus musculu
296	381	27.7	263	1	CPAD_RAT	P32038 rattus norv	369	352	25.6	277	2	Q7T0T6	Q7t0t6 xenopus lae
297	380.5	27.7	235	2	Q8N4E0	Q8n4e0 homo sapien	370	352	25.6	304	1	DISP_RAT	P33748 rattus norv
298	380	27.7	157	2	Q6B338	Q6b338 eumphyodon	371	352	25.6	505	2	Q96GV4	Q96gv4 halocynthia
299	380	27.6	455	2	Q7SY86	Q7sy86 xenopus lae	372	351.5	25.6	460	1	PRTC_MOUSE	P33587 mus musculu
300	379	27.6	261	2	Q8NCW4	Q8ncw4 homo sapien	373	351	25.5	310	1	DISP_MOUSE	Q9qy49 mus musculu
301	378	27.5	259	1	CPAD_MOUSE	Q6dhd3 brachydanio	374	351	25.5	456	1	PRTC_BOVIN	P00745 bos taurus
302	374.5	27.3	259	1	CPAD_MOUSE	P03953 mus musculu	375	350.5	25.5	265	2	Q804G1	Q804g1 brachydanio
303	372.5	27.1	261	2	Q6FHM3	Q6fhm3 homo sapien	376	350.5	25.5	274	2	Q16133	Q16133 anopheles s
304	372.5	27.1	261	2	Q8CFU4	Q8cfu4 rattus norv	377	350.5	25.5	274	2	Q17086	Q17086 anopheles s
305	371	27.0	271	1	EL2_RAT	P00774 rattus norv	378	350.5	25.5	434	2	Q7T3B6	Q7t3b6 brachydanio
306	370.5	27.0	204	2	Q86TV7	Q86tv7 homo sapien	379	350	25.5	263	2	Q6GPT1	Q6gpt1 homo sapien
307	370.5	27.0	259	1	CPAD_PIG	P51779 sus scrofa	380	350	25.5	268	2	Q6GQZ9	Q6gqz9 xenopus lae
308	370.5	27.0	263	1	CTR2_CANPA	P4813 canis famli	381	350	25.5	268	2	Q64Z88	Q64z88 xenopus tro
309	370	26.9	270	2	Q819P2	P63324 agkistrodon	382	350	25.5	271	2	Q18487	Q18487 peneaus van
310	370	26.9	270	2	Q819P2	Q819p2 aplousina fi	383	349.5	25.4	261	2	Q6FHW9	Q6fhw9 brachydanio
311	369	26.9	330	2	Q6NVW7	Q6nvw7 xenopus tro	384	349.5	25.4	269	1	EL2A_HUMAN	P08217 homo sapien
312	368.5	26.8	343	1	PS88_HUMAN	Q16651 homo sapien	385	349.5	25.4	269	2	Q6ICV2	Q6icv2 homo sapien
313	368	26.8	236	1	TRP3_PSSAM	Q93267 pseudopleur	386	349.5	25.4	277	2	Q96899	Q96899 scolopendra
314	368	26.8	418	1	HATT_HUMAN	O60235 homo sapien	387	349.5	25.4	371	2	Q8CJ16	Q8cj16 rattus norv
315	367.5	26.7	638	1	KAL_HUMAN	P33952 homo sapien	388	349.5	25.4	445	2	Q8CJ17	Q8cj17 rattus norv
316	366	26.6	258	1	VSP2_AGRCH	P47797 agkistrodon	389	349.5	25.4	558	2	Q6L7J1	Q6l7j1 rattus norv
317	366	26.6	260	2	Q9W7Q3	Q9w7q3 paratichthy	390	349.5	25.4	1130	2	Q7QIWT	Q7qim7 anopheles g
318	365.5	26.6	245	2	Q9XY60	Q9xy60 ctenocephal	391	349	25.4	1019	1	LFC_CARRO	Q26422 carcinoscor
319	365	26.6	263	2	Q7SAX7	Q7sax7 brachydanio	392	349	25.4	1083	2	Q264Z3	Q264z3 carcinoscor
320	363.5	26.5	339	2	Q99L44	Q99l44 mus musculu	393	348.5	25.4	429	2	Q8AYB0	Q8ayb0 brachydanio
321	363	26.4	340	2	Q8BVJ6	Q8bvj6 mus musculu	394	348.5	25.4	503	2	Q8AYB4	Q8ayb4 brachydanio
322	362.5	26.4	246	1	MCT1_MERUN	P50340 meriones un	395	348.5	25.4	799	2	Q6P94	Q6p94 mus musculu
323	362.5	26.4	387	2	Q9XY57	Q9xy57 ctenocephal	396	348.5	25.4	811	1	TMS6_MOUSE	Q9db10 mus musculu

397	348.5	25.4	818	2	06PRA6	Q6bba6 brachydanio	470	339.5	24.7	258	1	GRAM RAT	003238 rattus norv
398	348	25.3	267	2	TRV7_ANOGA	P35041 anopheles g	471	339.5	24.7	271	2	0803Z4	080324 brachydanio
399	348	25.3	269	2	Q6ISN8	Q6isn8 homo sapien	472	339.5	24.7	321	1	PLMN CANPA	P00009 canis famli
400	348	25.3	278	2	Q6PNF6	Q6pnf6 anopheles g	473	339.5	24.7	322	1	06IBE0	06iee0 rattus norv
401	347.5	25.3	344	2	Q640F8	Q640f8 xenopus lae	474	339	24.7	331	2	Q6VIF2	Q6vif2 mus musculu
402	347	25.3	275	2	Q6FHB8	Q6fhb8 homo sapien	475	339	24.7	335	2	Q6VIF2	Q6vif2 mus musculu
403	347	25.3	275	2	Q6FHB8	Q6fhb8 homo sapien	476	339	24.7	458	1	PRTC_RABIT	Q28661 oryctolagus
404	346.5	25.2	267	1	PRTC_HUMAN	P04070 homo sapien	477	339	24.7	461	1	FA9_HUMAN	P00740 homo sapien
405	346.5	25.2	267	1	Q9BK47	Q9bk47 luidia foli	478	339	24.7	625	1	FA9_PANTR	Q9nd47 pan troglod
406	346.5	25.2	354	2	EL2_BOVIN	Q29461 bos taurus	479	339	24.7	812	1	PLMN_HUMAN	001177 rattus norv
407	346.5	25.2	351	2	Q6IEK0	Q6ieko holotrichia	480	338.5	24.6	256	2	Q6VIF2	Q6vif2 mus musculu
408	346.5	25.2	435	1	TMS4_MOUSE	Q8vca5 mus musculu	481	338.5	24.6	258	1	EL1_HUMAN	018599 drosophila
409	346.5	25.2	435	1	Q9NPF2	Q9nfy2 anopheles g	482	338.5	24.6	258	2	Q6VIF2	Q6vif2 mus musculu
410	346.5	25.2	446	1	FA7_MOUSE	P70375 mus musculu	483	338.5	24.6	264	2	Q6ZND6	Q6znd6 culicx quing
411	346.5	25.2	446	1	Q7QC30	P70375 mus musculu	484	338.5	24.6	307	2	Q6ZND6	Q6znd6 mus sapien
412	346.5	25.2	441	1	PRTC_RAT	P31394 anopheles g	485	338.5	24.6	455	2	Q6CDR0	Q6cdr0 mus sapien
413	346.5	25.2	461	1	PRTC_RAT	Q6efy8 rattus norv	486	338.5	24.6	562	2	Q7PN85	Q7pn85 mus sapien
414	346.5	25.2	612	2	Q804W7	Q804w7 fugu rubrip	487	338.5	24.6	704	1	CRAR_MOUSE	Q01177 rattus norv
415	346	25.2	311	1	TRYG_MOUSE	Q9qu17 mus musculu	488	338.5	24.6	802	1	Q6UXD8	Q6uxd8 mus sapien
416	346	25.2	322	2	Q920S2	Q920s2 mus musculu	489	338	24.6	210	2	Q63Z11	Q63z11 mus sapien
417	345.5	25.1	454	2	Q46506	Q46506 papio hamad	490	338	24.6	365	2	Q97366	Q97366 mus sapien
418	345.5	25.1	467	2	Q667X8	Q667x8 panulirus a	491	338	24.6	382	2	Q44330	Q44330 holotrichia
419	345	25.1	253	1	TRV0_DROER	P54626 drosophila	492	338	24.6	418	2	Q7PGU3	Q44330 manduca sex
420	344.5	25.1	117	2	Q9PUF3	Q9puF3 bochrops ja	493	338	24.6	625	1	THRB_BOVIN	Q7pgu3 anopheles g
421	344.5	25.1	187	2	Q6PK75	Q6pk75 homo sapien	494	337.5	24.6	238	1	TRV5_AEDAE	P00735 bos taurus
422	344.5	25.1	275	2	Q6B051	Q6b051 homo sapien	495	337.5	24.6	261	2	Q6OX60	P29787 aedes aegy
423	344.5	25.1	855	2	Q7Z410	Q7z410 homo sapien	496	337.5	24.6	264	1	GRAM_HUMAN	Q6gx60 lepeophthei
424	344.5	25.1	1059	2	Q7Z411	Q7z411 homo sapien	497	337.5	24.6	282	2	Q9D4T3	Q9d4t3 mus sapien
425	344	25.0	257	2	Q8BZ04	Q8bz04 mus musculu	498	337.5	24.6	328	2	Q9DGR3	Q9dgr3 xenopus lae
426	344	25.0	265	2	Q6OX61	Q6ox61 lepeophthei	499	337.5	24.6	432	2	Q80Z40	Q80z40 rattus norv
427	344	25.0	275	1	TRB2_HUMAN	P20231 homo sapien	500	337.5	24.6	432	2	Q8CEP0	Q8cef0 mus musculu
428	344	25.0	282	2	Q6NZY1	Q6nzy1 homo sapien	501	337.5	24.6	471	2	Q8CEP0	Q8cef0 mus musculu
429	344	25.0	417	2	Q6BZ10	Q6bz10 mus musculu	502	337.5	24.5	247	2	Q17039	Q17039 anopheles g
430	343.5	25.0	266	2	Q46644	Q46644 macaca fasc	503	337	24.5	263	2	Q96RZ6	Q96rz6 mus sapien
431	343.5	25.0	273	2	MCT7_MOUSE	Q02844 mus musculu	504	337	24.5	275	2	Q96RZ6	Q96rz6 mus sapien
432	343.5	25.0	273	2	Q921N4	Q921n4 mus musculu	505	337	24.5	432	2	Q6UX37	Q6ux37 homo sapien
433	343.5	25.0	457	1	TMS5_HUMAN	Q931n4 mus musculu	506	337	24.5	434	1	UROK_CHICK	P15120 gallus galli
434	343	25.0	275	1	TRV7_CANPA	Q931n4 mus musculu	507	337	24.5	437	1	TMS4_HUMAN	Q931n4 gallus galli
435	343	25.0	284	2	Q8NFB6	P15944 canis famli	508	336.5	24.5	247	1	MCT1_PAPHA	Q931n4 mus sapien
436	343	25.0	318	2	Q7RTY9	Q7rt9 homo sapien	509	336.5	24.5	251	1	MCT3_SHEEP	P52195 papio hamad
437	342.5	24.9	248	2	Q16126	Q16126 boltenia vi	510	336.5	24.5	260	2	Q6P2V9	Q6p2v9 ovis aries
438	342.5	24.9	248	2	Q9XY52	Q9xy52 cleenoccephal	511	336.5	24.5	329	2	Q42272	Q42272 xenopus tro
439	342.5	24.9	271	2	Q8HY32	Q8hy32 bos taurus	512	336.5	24.5	428	2	Q8BPM7	Q8bpm7 mus sapien
440	342.5	24.9	273	1	MCT7_RAT	P27435 rattus norv	513	336.5	24.5	638	1	KAL_MOUSE	Q8bpm7 olkopleura
441	342.5	24.9	273	2	Q6P6W8	Q6p6w8 rattus norv	514	336	24.5	227	2	Q8X1T4	P26262 mus musculu
442	342.5	24.9	433	2	Q8JHD0	Q8jhd0 brachydanio	515	336	24.5	263	2	Q9DCR3	Q9dcr3 m mus muscu
443	342.5	24.9	517	2	Q90YK1	Q90yk1 brachydanio	516	336	24.5	263	2	Q9DCR3	Q9dcr3 m mus muscu
444	342.5	24.9	517	2	Q8KOD2	Q8kod2 mus musculu	517	336	24.5	273	1	TRYT_SHEEP	Q9dcr3 m mus muscu
445	342.5	24.9	624	1	FA11_MOUSE	Q91y47 mus musculu	518	336	24.5	280	2	Q64ID5	Q64id5 anthomomus
446	342.5	24.9	810	1	PLMN_HUMAN	P00747 homo sapien	519	336	24.5	402	2	Q7OB73	Q7ob73 anopheles g
447	342.5	24.9	811	1	TMS6_HUMAN	Q8iue0 homo sapien	520	336	24.5	416	1	FA9_BOVIN	P00741 bos taurus
448	342	24.9	275	1	TRB1_HUMAN	Q15661 homo sapien	521	336	24.5	485	2	Q7PKX0	Q7pkx0 anopheles g
449	342	24.9	355	2	Q7POR9	Q7por9 anopheles g	522	336	24.5	556	2	Q803D5	Q803d5 brachydanio
450	342	24.9	812	1	PLMN_MOUSE	P20918 mus musculu	523	336	24.5	654	2	Q6ONF4	Q6onf4 canis famli
451	341.5	24.9	258	1	GRAX_RAT	P49864 rattus norv	524	336	24.5	790	1	PLMN_PIG	P06867 sus scrofa
452	341.5	24.9	455	1	TMS5_MOUSE	Q9et04 rattus norv	525	335.5	24.4	258	1	Q6ISM6	Q6ism6 homo sapien
453	341.5	24.9	573	2	Q9V5T6	Q9v5t6 drosophila	526	335.5	24.4	265	1	TRV7_PIG	Q9v5t6 sus scrofa
454	341.5	24.9	1134	2	Q7RTT7	Q7rtt7 homo sapien	527	335.5	24.4	275	1	Q9VX7	Q9vx7 xenopus lae
455	341	24.8	251	2	Q9GLN2	Q9gln2 bos taurus	528	335.5	24.4	389	2	Q8VNF4	Q8vnf4 homo sapien
456	341	24.8	263	2	Q63ZK0	Q63zko xenopus lae	529	335.5	24.4	558	2	Q9UD19	Q9ud19 homo sapien
457	341	24.8	328	2	Q6IRA4	Q6ira4 xenopus lae	530	335	24.4	216	2	Q8MNY6	Q8mny6 mus sapien
458	341	24.8	572	2	Q7RTY8	Q7rt9 homo sapien	531	335	24.4	318	2	Q8MNY6	Q8mny6 mus sapien
459	341	24.8	719	2	Q6DJ90	Q6dj90 xenopus tro	532	335	24.4	433	2	Q8MNY6	Q8mny6 mus sapien
460	340.5	24.8	246	1	MCT4_MOUSE	P35035 anopheles g	533	335	24.4	701	2	Q9JTS9	Q9jts9 gallus galli
461	340.5	24.8	274	1	TRV1_ANOGA	Q8kx6 rattus norv	534	335	24.4	701	2	Q8CHN8	Q8chn8 rattus norv
462	340.5	24.8	446	1	FA7_RAT	Q9xcm1 mus musculu	535	334.5	24.3	247	2	Q70500	Q70500 mus musculu
463	340.5	24.8	624	2	Q9DAT3	Q9xcm1 ovis aries	536	334.5	24.3	263	1	GRAM_MOUSE	Q70500 mus musculu
464	340	24.7	273	2	Q9XSM1	Q9xsm1 mus sapien	537	334.5	24.3	275	2	Q7Y662	Q7y662 equus cabal
465	340	24.7	280	2	Q8N171	Q8n171 homo sapien	538	334.5	24.3	537	2	Q9BYE1	Q9bye1 homo sapien
466	340	24.7	297	2	Q8B781	Q8b781 anopheles g	539	334.5	24.3	581	2	Q9BYE2	Q9bye2 homo sapien
467	340	24.7	350	2	Q17489	Q17489 anopheles g	540	334	24.3	234	2	Q15096	Q15096 mus sapien
468	339.5	24.7	247	2	Q08732	Q08732 mesocricetu	541	334	24.3	264	2	Q8QGF6	Q8qgf6 xenopus lae
469	339.5	24.7	253	1	TRVY_DROER	P54625 drosophila	542	333.5	24.3	253	2	Q8MKZ1	Q8mkz1 drosophila

543	333.5	24.3	253	2	Q8SX24	Q8ex24 drosophila	616	328.5	23.9	365	2	Q7OLD1	Q7qld1 anopheles g
544	333.5	24.3	275	1	Q7PNF7	Q7pnf7 anopheles g	617	328.5	23.9	524	2	Q7SXH8	Q7exh8 brachydanio
545	333.5	24.3	290	2	PR27_HUMAN	Q8qrc7 homo sapien	618	328.5	23.9	615	2	Q6GNK4	Q6gnk4 xenopus lae
546	333.5	24.3	824	2	Q6ICG2	Q6icg2 homo sapien	619	328.5	23.9	681	2	Q7ZT70	Q7zt70 lampetra ja
547	333	24.2	245	1	CTRA_BOVIN	P00766 bos taurus	620	328.5	23.9	683	2	Q8MRH5	Q8mrh5 drosophila
548	333	24.2	256	1	Q9R0K0	Q9r0k0 mus musculu	621	328.5	23.9	786	1	STUB_DROME	Q05319 drosophila
549	333	24.2	285	1	FA9_CAVPO	P16295 cavia porce	622	328.5	23.9	787	2	Q9VEY6	Q9vey6 drosophila
550	333	24.2	320	2	Q7TDX2	Q7tdx2 xenopus lae	623	328	23.9	226	1	COGS_UCAPU	P00771 uca pugilat
551	333	24.2	355	2	Q7BWO0	Q7bwo0 anopheles g	624	328	23.9	328	2	Q6BRZ2	Q6brz2 rattus norv
552	333	24.2	360	2	Q7PEV7	Q7pev7 anopheles g	625	328	23.9	452	1	FA9_CANFA	P19540 canis famli
553	332.5	24.2	247	2	Q35342	Q35342 mesocricetu	626	328	23.9	767	2	Q9DGR2	Q9dgr2 xenopus lae
554	332.5	24.2	254	2	Q8T637	Q8t637 aedes aegyp	627	327.5	23.8	247	1	MCT1_MACFA	P56435 macaca fasc
555	332.5	24.2	260	2	Q8T4P6	Q8t4p6 lepeophthei	628	327.5	23.8	263	2	Q9TV16	Q9tv16 penaeus van
556	332.5	24.2	262	2	Q8T4P7	Q8t4p7 lepeophthei	629	327.5	23.8	266	2	Q27761	Q27761 penaeus van
557	332.5	24.2	263	2	Q7ZID5	Q7zid5 lepeophthei	630	327.5	23.8	269	2	Q96QV5	Q96qv5 homo sapien
558	332.5	24.2	264	2	Q7YSS9	Q7y89 lepeophthei	631	327.5	23.8	269	2	Q6ISM5	Q6ism5 homo sapien
559	332.5	24.2	490	1	TWS2_MOUSE	Q9j1q8 mus musculu	632	327.5	23.8	269	2	Q6GN82	Q6gn82 xenopus lae
560	332.5	24.2	638	1	KAL_RAT	P14272 rattus norv	633	327	23.8	263	1	DEF3_DERFA	P49275 dermatophag
561	332.5	24.2	810	1	PLMN_ERIEU	Q29485 erinaeus e	634	327	23.8	263	2	Q7SY64	Q7sy64 xenopus lae
562	332.5	24.2	810	1	PLMN_MACMU	P12545 macaca mula	635	327	23.8	270	2	Q27824	Q27824 uca pugilat
563	332	24.2	247	2	Q7OT74	Q7ot74 equus cabal	636	327	23.8	466	2	Q6SA95	Q6sa95 felis alive
564	332	24.2	251	2	Q7Q9W2	Q7q9w2 anopheles g	637	327	23.8	600	2	Q7ZTR2	Q7zt72 xenopus lae
565	332	24.2	258	2	Q97399	Q97399 phaeton coc	638	326.5	23.8	248	1	GRAC_MOUSE	P08882 mus musculu
566	332	24.2	266	2	Q92077	Q92077 gadus morhu	639	326.5	23.8	263	2	Q6GNF7	Q6gnf7 xenopus lae
567	332	24.2	277	2	Q8SQ44	Q8sq44 sus scrofa	640	326.5	23.8	266	1	EL1_PIG	P00772 sus scrofa
568	332	24.2	355	2	Q9NFU1	Q9nful anopheles g	641	326.5	23.8	266	2	Q91X79	Q91x79 mus musculu
569	331.5	24.1	254	2	Q8MT4P4	Q8mt4p4 lepeophthei	642	326.5	23.8	369	2	Q7QK11	Q7qk11 anopheles g
570	331.5	24.1	254	2	Q8MMK9	Q8mmk9 aedes aegyp	643	326.5	23.8	490	2	Q7TNO4	Q7tno4 mus musculu
571	331.5	24.1	256	1	TRYA_DROME	P04814 drosophila	644	326	23.7	248	1	GRZ1_RAT	Q06605 rattus norv
572	331.5	24.1	260	2	Q8T4P5	Q8t4p5 lepeophthei	645	326	23.7	271	1	CTR2_PENVA	P36178 penaeus van
573	331.5	24.1	263	2	Q9PMQ6	Q9pmq6 gadus morhu	646	326	23.7	329	2	Q7PEV8	Q7pev8 anopheles g
574	331.5	24.1	264	2	Q6GPM5	Q6gpm5 xenopus lae	647	326	23.7	432	2	Q7QK14	Q7qk14 anopheles g
575	331.5	24.1	275	1	TRV3_ANOCA	P35037 anopheles g	648	325.5	23.7	259	2	Q8IRE0	Q8ire0 drosophila
576	331	24.1	263	1	CTRB_RAT	P00734 rattus norv	649	325.5	23.7	261	1	DER3_DERPT	P39675 dermatophag
577	331	24.1	622	1	THRB_HUMAN	Q7z7p3 homo sapien	650	325.5	23.7	268	2	Q46151	Q46151 pacifastacu
578	331	24.1	722	2	Q8AW90	Q8aw90 lampetra ja	651	325.5	23.7	306	1	BSS4_MOUSE	Q9er10 mus musculu
579	331	24.1	722	2	Q9PSZ5	Q9psz5 lampetra ja	652	325.5	23.7	891	2	Q9VV38	Q9vv38 drosophila
580	331	24.1	722	1	Q9PSZ5	P23946 homo sapien	653	324.5	23.6	146	2	Q9DD81	Q9dde1 brachydanio
581	330.5	24.1	247	1	TRYA_HUMAN	P54624 drosophila	654	324.5	23.6	228	2	Q7O153	Q7o153 anopheles g
582	330.5	24.1	256	1	TRV1_DROER	Q518p3 homo sapien	655	324.5	23.6	263	2	Q7PUB9	Q7pub9 drosophila
583	330.5	24.1	269	2	Q6ISP9	Q6isp9 homo sapien	656	324.5	23.6	275	1	TRYA_HUMAN	P39675 dermatophag
584	330.5	24.1	560	2	Q14520	Q14520 homo sapien	657	324.5	23.6	391	2	Q9V322	Q9v322 drosophila
585	330.5	24.1	638	2	Q8R0P5	Q8r0p5 mus musculu	658	324	23.6	253	1	TRVB_DROME	P15157 homo sapien
586	330	24.0	236	2	Q7SIG3	Q7sig3 balmo saliar	659	324	23.6	257	1	GRAM_HUMAN	P51124 homo sapien
587	330	24.0	253	2	Q9V5Y3	Q9v5y3 drosophila	660	324	23.6	266	2	Q9W7Q0	Q9w7q0 paratichthy
588	330	24.0	266	2	Q8I916	Q8i916 biomia trop	661	324	23.6	459	1	FA9_MOUSE	P16294 mus musculu
589	330	24.0	282	1	FA9_RAT	P16296 rattus norv	662	324	23.6	277	2	ENTR_HUMAN	P88073 homo sapien
590	330	24.0	4548	1	APQA_HUMAN	Q29464 bos taurus	663	323.5	23.5	277	2	Q9VSB7	Q9vsb7 mus musculu
591	329.5	24.0	237	2	Q29464	Q29464 bos taurus	664	323.5	23.5	299	2	Q9VSB7	Q9vsb7 mus musculu
592	329.5	24.0	248	1	O8T4P2	P842p2 lepeophthei	665	323.5	23.5	328	2	Q8BJR6	Q8bjr6 mus musculu
593	329.5	24.0	253	1	TRYD_DROME	P42276 drosophila	666	323.5	23.5	466	1	PA7_HUMAN	P88709 homo sapien
594	329.5	24.0	262	2	Q7ZID6	Q7zid6 lepeophthei	667	323.5	23.5	490	2	Q6PTD7	Q6ptd7 rattus norv
595	329.5	24.0	266	2	Q8WR10	Q8wr10 paratichode	668	323.5	23.5	608	1	Q9PTW7	Q9ptw7 etruthio ca
596	329.5	24.0	269	1	BL2B_HUMAN	P08218 homo sapien	669	323.5	23.5	875	2	NETR_HUMAN	P66730 homo sapien
597	329.5	24.0	320	2	Q7PEV6	Q7pev6 anopheles g	670	323	23.5	281	2	Q46137	Q46137 lumbricue x
598	329.5	24.0	578	2	Q6O017	Q6o017 bos taurus	671	323	23.5	296	2	Q9VDV1	Q9vdv1 drosophila
599	329.5	24.0	1420	1	APQA_MACMU	P14417 macaca mula	672	323	23.5	540	2	Q8O0V7	Q8o0v7 drosophila
600	329	23.9	216	1	VSPB_LACMU	P84036 lacheis mu	673	323	23.5	653	1	HGFA_MOUSE	Q9r038 mus musculu
601	329	23.9	264	1	Q08643	Q08643 mus musculu	674	323	23.5	653	2	Q8VCS4	Q8vcs4 mus musculu
602	329	23.9	279	2	Q9NMG4	Q9nmg4 mus musculu	675	322.5	23.5	249	2	Q6OX62	Q6ox62 lepeophthei
603	329	23.9	307	2	Q7TMO0	Q7tmo0 mus musculu	676	322.5	23.5	258	2	Q9W5U8	Q9w5u8 drosophila
604	329	23.9	572	2	Q8BIK6	Q8bik6 mus musculu	677	322.5	23.5	324	1	TEST_MOUSE	Q9jhi7 mus musculu
605	329	23.9	575	2	Q7Q9W3	Q7q9w3 anopheles g	678	322.5	23.5	336	2	Q8OYD8	Q8oyd8 mus musculu
606	329	23.9	722	2	Q8NDU5	Q8ndu5 xenopus lae	679	322.5	23.5	372	2	Q9Y1K6	Q9y1k6 anopheles g
607	328.5	23.9	235	1	O8T4P3	Q8t4p3 lepeophthei	680	322.5	23.4	581	2	Q9XZM7	Q9xzm7 etrongyloce
608	328.5	23.9	245	1	CTRB_GADMO	P80646 gadus morhu	681	322	23.4	210	2	Q68DS2	Q68ds2 homo sapien
609	328.5	23.9	253	1	TRYG_DROME	P42277 drosophila	682	322	23.4	699	1	CRAR_HUMAN	P48740 h complemen
610	328.5	23.9	260	1	MCT1_RAT	P09650 rattus norv	683	322	23.4	1303	2	Q66SB4	Q66sb4 olkopleura
611	328.5	23.9	261	2	O8T4P1	Q8t4p1 lepeophthei	684	321.5	23.4	263	2	Q6Z562	Q6z562 penaeus van
612	328.5	23.9	275	2	O8ETW8	Q8etw8 homo sapien	685	321.5	23.4	265	2	Q7SY18	Q7sy18 xenopus lae
613	328.5	23.9	276	2	Q86DU5	Q86du5 homo sapien	686	321.5	23.4	266	2	Q9D936	Q9d936 mus musculu
614	328.5	23.9	338	1	PLMN_HORSE	P80010 equus cabal	687	321.5	23.4	679	2	Q96PQ8	Q96pq8 homo sapien
615	328.5	23.9	364	2	Q9NAB9	Q9nas9 anopheles g	688	321	23.4	226	1	DDN1_BOVIN	P80219 bos taurus

689	321	23.4	230	2	06IE13	06IE13	rattus norv	762	314	22.9	629	2	06AZS7	06AZS7	xenopus lae
690	321	23.4	247	1	MCT2	MERUN	meriones un	763	314	22.9	855	1	ST14	HUMAN	09Y516
691	321	23.4	248	1	NKPI	RAT	rattus norv	764	313.5	22.8	261	1	EUM3	EURMA	09Y370
692	321	23.4	269	1	TRVM	CANPA	canis famli	765	313.5	22.8	321	2	080Y38		080Y38
693	321	23.4	411	2	09VU10		09VU10	766	313.5	22.8	326	2	09D9M0		09D9M0
694	321	23.4	655	1	HEFA	HUMAN	004756	767	313.5	22.8	364	2	0917V4		0917V4
695	320.5	23.3	247	1	GRAB	MOUSE	004187	768	313.5	22.8	425	2	0804X7		0804X7
696	320.5	23.3	312	2	07M755		07M755	769	313	22.8	241	2	0917I2		0917I2
697	320	23.3	249	2	09W701		09W701	770	313	22.8	336	2	08CIR9		08CIR9
698	320	23.3	489	2	07Q432		07Q432	771	313	22.8	420	2	090504		090504
699	320	23.3	536	2	07PXR2		07PXR2	772	313	22.8	613	2	003711		003711
700	319.5	23.3	265	2	06GNG0		06GNG0	773	313	22.8	697	2	08CG43		08CG43
701	319.5	23.3	559	2	06P7U0		06P7U0	774	313	22.8	733	2	0920S0		0920S0
702	319.5	23.3	607	2	06DF05		06DF05	775	313	22.8	732	2	08CD27		08CD27
703	319	23.2	241	2	07PEP7		07PEP7	776	313	22.8	835	2	09U1I7		09U1I7
704	319	23.2	264	2	08IPY7		08IPY7	777	312.5	22.7	241	2	081Y12		081Y12
705	319	23.2	270	2	064ID1		064ID1	778	312.5	22.7	271	2	08T9R6		08T9R6
706	319	23.2	320	2	08CIR7		08CIR7	779	312.5	22.7	274	1	TRYS	ANOGA	08T9R6
707	319	23.2	461	2	095ND6		095ND6	780	312.5	22.7	300	2	096RF3		096RF3
708	319	23.2	1034	1	ENTK	PIG	095nd6	781	312.5	22.7	390	2	09Y157		09Y157
709	318.5	23.2	343	1	PLMN	SHEEP	098074	782	312.5	22.7	615	1	PA12	HUMAN	09Y157
710	318.5	23.2	418	2	06IE15		06IE15	783	312.5	22.7	680	2	086BHS		086BHS
711	318.5	23.2	490	2	0920K3		0920K3	784	312.5	22.7	1234	2	07PIQ7		07PIQ7
712	318	23.1	232	2	094508		094508	785	312.5	22.7	1332	2	07PWR7		07PWR7
713	318	23.1	258	2	07YRZ7		07YRZ7	786	312.5	22.7	1332	2	09NUS5		09NUS5
714	318	23.1	261	2	0962G7		0962G7	787	312	22.7	295	2	08CIP7		08CIP7
715	318	23.1	265	2	018488		018488	788	312	22.7	374	2	081B62		081B62
716	318	23.1	271	1	FA9	PIG	096297	789	312	22.7	597	2	035727		035727
717	318	23.1	274	1	FA9	SHEEP	096297	790	312	22.7	609	2	06PER0		06PER0
718	318	23.1	295	2	069EZ8		069EZ8	791	311.5	22.7	255	2	025227		025227
719	318	23.1	618	1	THRB	MOUSE	099x21	792	311.5	22.7	255	2	07NTI0		07NTI0
720	317.5	23.1	245	1	CTRB	BOVIN	099x21	793	311.5	22.7	293	2	023528		023528
721	317.5	23.1	246	1	GRAN	BOVIN	099x21	794	311.5	22.7	566	1	TPA	BOVIN	099x21
722	317.5	23.1	248	2	09YX9		09YX9	795	311.5	22.7	645	1	TPME4		TPME4
723	317.5	23.1	256	1	TRYE	DROER	099x21	796	311.5	22.7	761	1	NETR	MOUSE	099x21
724	317.5	23.1	559	2	09VUG2		09VUG2	797	311.5	22.7	1222	2	09NATO		09NATO
725	317.5	23.1	604	1	CPAI	MOUSE	099x21	798	311.5	22.7	249	2	06IE11		06IE11
726	317.5	23.1	617	2	08T151		08T151	799	311	22.6	250	2	09V514		09V514
727	317.5	23.1	248	2	063636		063636	800	311	22.6	261	1	CARG	MOUSE	09V514
728	317	23.1	624	2	095ME7		095ME7	801	311	22.6	431	1	ACRO	RABIT	09V514
729	317	23.1	441	2	MCT1	MOUSE	095ME7	802	311	22.6	433	1	UROK	BOVIN	09V514
730	316.5	23.0	246	1	081917		081917	803	311	22.6	1035	1	ENTK	BOVIN	09V514
731	316.5	23.0	607	2	091001		091001	804	311	22.6	1042	1	CORT	HUMAN	09V514
732	316.5	23.0	246	2	09YX46		09YX46	805	310.5	22.6	257	2	MCT2	RAT	09YX46
733	316	23.0	259	2	069EZ7		069EZ7	806	310.5	22.6	299	2	07PEF7		07PEF7
734	316	23.0	263	2	002570		002570	807	310.5	22.6	371	2	08MRV3		08MRV3
735	316	23.0	269	2	09CQ52		09CQ52	808	310.5	22.6	473	2	TPV63		TPV63
736	316	23.0	269	2	09D779		09D779	809	310.5	22.6	559	1	TPA	RAT	TPV63
737	316	23.0	254	1	TRY3	AEDAB	099766	810	310.5	22.6	1374	2	QVSVU0		QVSVU0
738	315.5	23.0	264	2	062561		062561	811	310.5	22.6	1449	2	09U1I2		09U1I2
739	315.5	23.0	265	2	066KR6		066KR6	812	310.5	22.6	1450	2	0810B8		0810B8
740	315.5	23.0	266	1	ELI	RAT	066KR6	813	310.5	22.6	1462	2	09U1I3		09U1I3
741	315.5	23.0	314	2	QVVR15		QVVR15	814	310.5	22.6	2382	2	09B1I9		09B1I9
742	315.5	23.0	314	2	Q7QC55		Q7QC55	815	310.5	22.6	2409	2	0960G6		0960G6
743	315.5	23.0	453	1	EAST	DROME	0960G6	816	310.5	22.6	2786	2	QVSVU2		QVSVU2
744	315.5	23.0	453	1	0812A6		0812A6	817	310.5	22.6	275	1	FA9	RABIT	0812A6
745	315.5	23.0	492	1	FA10	BOVIN	0960G6	818	310	22.6	327	2	070530		070530
746	315.5	23.0	248	2	063224		063224	819	310	22.6	483	2	08T8X4		08T8X4
747	315	22.9	280	2	066NK6		066NK6	820	310	22.6	483	2	QVXK10		QVXK10
748	315	22.9	323	2	096Q44		096Q44	821	310	22.6	1111	2	080YV4		080YV4
749	315	22.9	617	1	THRB	RAT	096Q44	822	309.5	22.5	246	2	09EPR0		09EPR0
750	315	22.9	686	1	MAS2	HUMAN	096Q44	823	309.5	22.5	255	2	09Y7A9		09Y7A9
751	315	22.9	256	1	TRYE	DROME	096Q44	824	309.5	22.5	265	2	09VVR3		09VVR3
752	314.5	22.9	261	2	06IDF4		06IDF4	825	309.5	22.5	284	2	070493		070493
753	314.5	22.9	283	1	TMS3	MOUSE	06UWY2	826	309.5	22.5	482	1	PA10	RAT	06UWY2
754	314.5	22.9	453	1	07M761		07M761	827	309.5	22.5	868	2	09Y1V3		09Y1V3
755	314.5	22.9	609	2	086BH7		086BH7	828	309	22.5	285	2	08CG42		08CG42
756	314.5	22.9	680	2	0868H7		0868H7	829	309	22.5	404	2	070XK2		070XK2
757	314.5	22.9	275	1	TRY4	ANOGA	0868H7	830	308.5	22.5	240	2	06IE06		06IE06
758	314	22.9	280	2	070454		070454	831	308.5	22.5	246	1	MCT9	MOUSE	070454
759	314	22.9	280	2	066NK5		066NK5	832	308.5	22.5	260	2	06VPI6		06VPI6
760	314	22.9	422	2	08WVC1		08WVC1	833	308	22.4	125	2	0804G0		0804G0
761	314	22.9						834	308	22.4					

835	308	22.4	300	2	OB19P4	OB19P4 aurelia aur	908	302	22.0	269	2	Q7PW17	Q7PW17 anopheles g
836	308	22.4	317	1	BSS4_HUMAN	Ogexn4 homo sapien	909	302	22.0	321	2	O6MZL2	O6MZL2 homo sapien
837	308	22.4	334	2	O6UXE0	O6uxd2 homo sapien	910	302	22.0	394	1	URTG_DESRO	P9150 desmodus ro
838	308	22.4	335	2	O6EPB3	O6epb3 drosophila	911	302	22.0	477	1	URT2_DESRO	P15638 desmodus ro
839	308	22.4	377	2	O9VB68	O9vb68 drosophila	912	301.5	21.9	241	2	O8BW11	O8bw11 m mus muscu
840	308	22.4	408	2	O9MR95	O9mr95 drosophila	913	301.5	21.9	394	2	P91817	P91817 tachypleus
841	308	22.4	698	2	O6GPF9	O6gpf9 xenopus lae	914	301.5	21.9	505	2	O7QCW2	O7qcw2 anopheles g
842	307.5	22.4	255	2	O7PFI6	O7pfi6 anopheles g	915	301	21.9	255	1	CATG_HUMAN	P08311 homo sapien
843	307.5	22.4	471	2	O804X6	O804x6 gallus gall	916	301	21.9	255	2	O342E9	O342e9 salvelinus
844	307.5	22.4	676	2	O6DUU6	O6duu6 cyprinus ca	917	301	21.9	278	2	O17030	O17030 anopheles g
845	307	22.3	135	2	O62284	O62284 mus musculu	918	301	21.9	279	2	O7PXJ9	O7pxj9 anopheles g
846	307	22.3	250	2	O17036	O17036 anopheles g	919	301	21.9	279	2	O7TNX3	O7tnx3 mus musculu
847	307	22.3	259	1	CTRI_ANOGA	O27289 anopheles g	920	301	21.9	283	2	O9SV22	O9sv22 lumbricus b
848	307	22.3	318	2	O7Q9M4	O7q9m4 anopheles g	921	301	21.9	417	2	O8VHK8	O8vhk8 mus musculu
849	307	22.3	417	1	HEPS_HUMAN	P05981 homo sapien	922	301	21.9	417	2	O8VDV1	O8vdv1 mus musculu
850	307	22.3	726	2	O7QBP4	O7qbp4 anopheles g	923	301	21.9	431	1	URTB_DESRO	P8121 desmodus ro
851	306.5	22.3	368	2	O9W454	O9w454 drosophila	924	301	21.9	728	2	O96RS4	O96rs4 homo sapien
852	306.5	22.3	365	2	O7QGL1	O7qgl1 anopheles g	925	300.5	21.9	239	2	O7T2H1	O7t2h1 xenopus lae
853	306.5	22.3	375	1	PCE_TACTR	P21902 tachypleus	926	300.5	21.9	276	2	P91894	P91894 arenicola m
854	306.5	22.3	418	2	O8SZK2	O8szk2 drosophila	927	300.5	21.9	278	2	O68FW6	O68fw6 brachydanio
855	306.5	22.3	468	2	O9UOC3	O9uoc3 pacifastacu	928	300.5	21.9	386	2	O81924	O81924 bombyx mori
856	306	22.3	162	2	O6UBM2	O6ubm2 homo sapien	929	300.5	21.9	424	2	O9VAB8	O9vab8 drosophila
857	306	22.3	247	2	O8NID2	O8nid2 homo sapien	930	300.5	21.9	433	2	O8MHY7	O8mhy7 oryctolagus
863	305.5	22.2	256	1	HYPA_HYPLI	P35587 hypoderma 1	936	300	21.8	291	2	O8VHJ4	O8vhj4 rattus norv
864	305.5	22.2	274	2	O6GNFO	O6gnfo xenopus lae	937	300	21.8	417	2	O9PU71	O9pu71 xenopus lae
865	305.5	22.2	383	2	O77102	O77102 manduca sex	938	300	21.8	698	2	O9PU71	O9pu71 rattus norv
866	305.5	22.2	418	2	O9VAB7	O9vab7 drosophila	939	299.5	21.8	241	2	O63637	O63637 rattus norv
867	305.5	22.2	441	2	O804X2	O804x2 figu rubrip	940	299.5	21.8	246	1	MCTX_MOUSE	O00356 mus musculu
868	305	22.2	247	1	GRAB_HUMAN	P10144 h giranzyme	941	299.5	21.8	254	2	O6DSB8	O6dsb8 brachydanio
869	305	22.2	281	2	O67BC3	O67bc3 homo sapien	942	299.5	21.8	257	2	O19023	O19023 macaca mula
870	305	22.2	307	2	O64ID2	O64id2 anthomus	943	299.5	21.8	258	1	CTR2_ANOGA	O17025 anopheles g
871	305	22.2	391	2	O7PKJ5	O7pkj5 anopheles g	944	299.5	21.8	272	2	O7Q9W5	O7q9w5 anopheles g
872	305	22.2	395	2	O9BZM1	O9bzm1 homo sapien	945	299.5	21.8	282	2	O7PTI6	O7pti6 anopheles g
873	305	22.2	532	2	O7PX73	O7px73 anopheles g	946	299.5	21.8	325	2	O15944	O15944 sarcophaga
874	304.5	22.2	258	2	O9XY53	O9xy53 ctenocephal	947	299.5	21.8	372	2	O9WZC8	O9wzc8 drosophila
875	304.5	22.2	271	2	O7Q820	O7q820 anopheles g	948	299.5	21.8	430	2	O6RU03	O6ru03 trichinella
876	304.5	22.2	384	2	O9XY63	O9xy63 ctenocephal	949	299.5	21.8	436	1	ACRO_MOUSE	P35758 mus musculu
877	304.5	22.2	492	1	TMS2_HUMAN	O15393 homo sapien	950	299.5	21.8	465	2	O9BUL7	O9bul7 trichinella
878	304.5	22.2	492	1	O96T73	O96t73 homo sapien	951	299.5	21.8	615	2	O81Z25	O81z25 homo sapien
879	304	22.1	268	1	CLCR_HUMAN	O99895 homo sapien	952	299.5	21.8	974	2	O90WD8	O90wd8 bufo japoni
880	304	22.1	272	2	O9XYV6	O9xyv6 thyzopeterha	953	299.5	21.8	1069	1	ENTX_MOUSE	P97435 mus musculu
881	304	22.1	375	2	O817W8	O817w8 dermacentor	954	299	21.8	256	2	O6VIQ1	O6viq1 verticilliu
882	304	22.1	393	2	O6RX66	O6rx66 armigeres s	955	299	21.8	437	1	ACRO_RAT	P29293 rattus norv
883	304	22.1	400	2	O9VCJ8	O9vcj8 drosophila	956	298.5	21.7	235	2	O91004	O91004 gecko gecko
884	304	22.1	423	2	O8BM10	O8bm10 mus musculu	957	298.5	21.7	248	1	O9VO98	O9v098 drosophila
885	304	22.1	543	2	O9BU59	O9bu59 homo sapien	958	298.5	21.7	249	1	MCT1_CANFA	P31842 canis famli
886	304	22.1	562	1	TPA_HUMAN	P00750 homo sapien	959	298.5	21.7	350	2	O7OKT0	O7okt0 anopheles g
887	304	22.1	589	2	O6PJ55	O6pja5 homo sapien	960	298.5	21.7	407	1	FAT_BOVIN	P22457 bos taurus
888	304	22.1	685	2	O9Z338	O9z338 mus musculu	961	298.5	21.7	433	2	O8T3A2	O8t3a2 cioba teneb
889	304	22.1	1379	2	O9V4N6	O9v4n6 drosophila	962	298.5	21.7	733	2	O9VTX9	O9vtx9 drosophila
890	304	22.1	1397	2	O7KQO9	O7kqg9 drosophila	963	298	21.7	235	2	O28731	O28731 oryctolagus
891	303.5	22.1	240	2	O7SIO8	O7byg6 xenopus lae	964	298	21.7	255	2	O18435	O18435 helicoverpa
892	303.5	22.1	244	1	MCT2_MOUSE	P15119 mus musculu	965	298	21.7	268	2	O8T474	O8t474 aedes aegypt
893	303.5	22.1	246	1	MCT4_RAT	P91592 rattus norv	966	298	21.7	348	2	O86W55	O86w55 homo sapien
894	303.5	22.1	278	2	O7Q492	O7q492 anopheles g	967	297.5	21.7	254	2	O76520	O76520 stomoxys ca
895	303.5	22.1	309	2	O27083	O27083 tachypleus	968	297.5	21.7	256	2	O6MJY6	O6mjy6 bdellovibri
896	303.5	22.1	603	1	CFAT_MOUSE	O61125 mus musculu	969	297.5	21.7	269	2	O6AZP9	O6azp9 xenopus lae
897	303.5	22.1	761	2	O9JUC8	O9juc8 rattus norv	970	297.5	21.7	277	2	O8IQ10	O8iq10 drosophila
898	303	22.1	246	1	MCT2_SHEEP	P93204 ovis aries	971	297.5	21.7	293	2	O7Q8P9	O7q8p9 anopheles g
899	303	22.1	259	2	O6JPF5	O6jpf5 neodiprion	972	297.5	21.7	408	2	O9VW19	O9vw19 drosophila
900	302.5	22.0	223	2	O9NR68	O9nr68 homo sapien	973	297.5	21.7	435	1	SNAK_DROME	P50049 drosophila
901	302.5	22.0	273	1	TRY6_Y4	O9vby4 drosophila	974	297.5	21.7	472	2	O7O1B2	O7o1b2 anopheles g
902	302.5	22.0	1004	2	P79953	P79953 anopheles g	975	297.5	21.7	486	2	O7PX74	O7px74 anopheles g
903	302.5	22.0	1004	2	P79953	P79953 xenopus lae	976	297.5	21.7	519	2	O8T3A3	O8t3a3 cioba teneb
904	302.5	22.0	1113	1	CORI_MOUSE	O9z319 mus musculu	977	297.5	21.7	616	2	O97507	O97507 sus scrofa
905	302	22.0	247	2	O6T376	O6t376 elisbenia foe	978	297	21.6	237	1	TRYP_ASTFL	P00765 atacus flu
906	302	22.0	255	1	TRY4_LUCCU	P35044 lucilia cup	979	297	21.6	247	1	MCT5_MOUSE	P21844 mus musculu
907	302	22.0	268	2	O9W7Q2	O9w7q2 paratitichy	980	297	21.6	256	2	O9XY51	O9xy51 ctenocephal

981	297	21.6	268	2	Q9B1G0	Q9b1g0 aedes aegyp	1054	291.5	21.2	270	2	Q7Q5A6	Q7q5a6 anopheles g
982	297	21.6	284	2	Q81RX5	Q81rx5 drosophila	1055	291	21.2	239	2	Q6LCU4	Q6lcu4 lumbricus r
983	297	21.6	352	2	Q6URM4	Q6urmd homo sapien	1056	291	21.2	239	2	Q542J3	Q542j3 streptomyce
984	297	21.6	369	2	Q6AXZ6	Q6axz6 rattus norv	1057	291	21.2	436	1	HEPS_MOUSE	Q54543 mus musculu
985	297	21.6	454	1	TW53_HUMAN	P57727 homo sapien	1058	291	21.2	678	2	Q3U5E8	Q3u5e8 rattus norv
986	297	21.6	477	1	UR11_DESRO	P58119 desmodus ro	1059	290.5	21.1	483	2	Q7PKJ7	Q7pkj7 anopheles g
987	296.5	21.6	248	1	GRAF_MOUSE	P08883 mus musculu	1060	290.5	21.1	681	2	Q7Q554	Q7q554 anopheles g
988	296.5	21.6	270	1	EL3B_HUMAN	P08861 homo sapien	1061	290	21.1	256	1	HYPB_HYPLI	Q65y8 hypodermia 1
989	296.5	21.6	272	2	Q9V5X6	Q9v5x6 drosophila	1062	290	21.1	256	1	Q6D7Y8	Q6d7y8 hypodermia 1
990	296.5	21.6	273	2	Q9V5X6	Q9v5x6 drosophila	1063	290	21.1	257	2	Q274A0	Q274a0 aedes aegyp
991	296.5	21.6	581	2	Q960I5	Q960i5 drosophila	1064	290	21.1	350	2	Q819Z7	Q819z7 hyphantria
992	296.5	21.6	1047	2	Q9V2H2	Q9v2h2 drosophila	1065	289.5	21.1	246	2	Q9BLI7	Q9bli7 lumbricus r
993	296	21.5	265	2	Q9V2H2	Q9v2h2 drosophila	1066	289.5	21.1	257	2	Q6RS60	Q6rs60 ostrinia nu
994	296	21.5	279	2	Q9QZ74	Q9qz74 rattus norv	1067	289.5	21.1	257	2	Q6RS60	Q6rs60 ostrinia nu
995	296	21.5	281	2	Q9QZ74	Q9qz74 rattus norv	1068	289.5	21.1	257	2	Q6RS60	Q6rs60 ostrinia nu
996	296	21.5	314	2	Q6RUT2	Q6rut2 mus musculu	1069	289	21.0	260	2	Q7RRY3	Q7rry3 homo sapien
997	296	21.5	318	2	Q8OUR4	Q8our4 mus musculu	1070	289	21.0	278	2	Q7OHS0	Q7ohs0 anopheles g
998	295.5	21.5	229	2	Q9GME0	Q9gme0 ornithorhyn	1071	289	21.0	339	2	Q9OX91	Q9ox91 anopheles g
999	295.5	21.5	239	2	Q912I8	Q912i8 oncorhynch	1072	289	21.0	366	2	Q9QX85	Q9qx85 anopheles g
1000	295.5	21.5	270	2	Q9VRS4	Q9vrs4 drosophila	1073	289	21.0	376	1	FA10_TROCA	FA10 troca
1001	295.5	21.5	433	1	Q9VRS4	Q9vrs4 drosophila	1074	289	21.0	441	1	Q9XXV0	Q9xxv0 rattus norv
1002	295.5	21.5	449	2	Q9VDU8	Q9vdu8 drosophila	1075	289	21.0	541	2	Q9QX90	Q9qx90 rattus norv
1003	295.5	21.5	453	2	Q6ZMC3	Q6zmc3 homo sapien	1076	289	21.0	583	1	CFAL_HUMAN	CFal human
1004	295	21.5	260	2	Q9VCP6	Q9vcp6 drosophila	1077	289	21.0	623	2	Q9JUE3	Q9jue3 ctenocephal
1005	295	21.5	267	2	Q6DGM4	Q6dgm4 brachydanio	1078	289	21.0	643	2	Q9OX84	Q9ox84 rattus norv
1006	295	21.5	268	2	Q81RT5	Q81rt5 aedes aegyp	1079	288.5	21.0	255	2	Q9XK62	Q9xk62 ctenocephal
1007	295	21.5	269	2	Q95KM7	Q95km7 bos taurus	1080	288.5	21.0	264	2	Q7Q290	Q7q290 anopheles g
1008	295	21.5	358	2	Q450Z9	Q450z9 aedes aegyp	1081	288.5	21.0	315	2	Q81R33	Q81r33 drosophila
1009	295	21.5	553	2	Q6P7I9	Q6p7i9 xenopus lae	1082	288.5	21.0	438	2	Q6ZK41	Q6zk41 mus musculu
1010	294.5	21.4	244	2	Q81R63	Q81r63 drosophila	1083	288.5	21.0	442	2	Q804X1	Q804x1 fuju rubrip
1011	294.5	21.4	575	2	Q81R63	Q81r63 drosophila	1084	288.5	21.0	1047	2	Q240I9	Q240i9 drosophila
1012	294	21.4	247	2	Q61E57	Q61e57 rattus norv	1085	288	21.0	257	2	Q9NBA9	Q9nba9 aedes aegyp
1013	294	21.4	259	2	Q9XYF1	Q9xyf1 ctenocephal	1086	288	21.0	261	2	Q81RE1	Q81re1 drosophila
1014	294	21.4	265	2	Q9VHF8	Q9vfh8 drosophila	1087	288	21.0	405	2	Q8WZM7	Q8wzm7 anopheles g
1015	294	21.4	271	2	Q9GTX2	Q9gtx2 lumbricus r	1088	288	21.0	421	2	Q7PEY0	Q7pey0 anopheles g
1016	294	21.4	283	2	Q25394	Q25394 lumbricus r	1089	288	21.0	405	2	Q6Q491	Q6q491 cavia porce
1017	294	21.4	283	2	Q81RT7	Q81rt7 lumbricus r	1090	288	21.0	730	2	Q601O8	Q601o8 gallus gall
1018	294	21.4	293	2	Q7Z5A4	Q7z5a4 homo sapien	1091	287.5	20.9	234	2	Q9G2A4	Q9g2a4 gallus gall
1019	294	21.4	303	2	Q7E900	Q7e900 drosophila	1092	287.5	20.9	244	2	Q6T375	Q6t375 acipenser t
1020	293.5	21.4	246	2	Q61E10	Q61e10 rattus norv	1093	287.5	20.9	472	2	Q61GR2	Q61gr2 drosophila
1021	293.5	21.4	256	2	Q9XYV1	Q9xyv1 rhizopertha	1094	287.5	20.9	249	2	Q7RRD0	Q7rrd0 drosophila
1022	293.5	21.4	257	2	Q7Z0G1	Q7z0g1 phlebotomus	1095	287.5	20.9	603	1	FA12_CAVPO	FA12 cavpo
1023	293.5	21.4	302	2	Q8SYZ7	Q8syz7 drosophila	1096	287.5	20.9	845	2	Q63Z06	Q63z06 xenopus lae
1024	293.5	21.4	302	2	Q9W5E6	Q9w5e6 drosophila	1097	287.5	20.9	204	2	Q6S9W8	Q6s9w8 homo sapien
1025	293.5	21.4	431	1	UROC_HUMAN	P00749 homo sapien	1098	287	20.9	244	2	Q6S9W8	Q6s9w8 homo sapien
1026	293.5	21.4	845	1	Q6GR54	Q6gr54 xenopus lae	1099	287	20.9	256	2	Q25081	Q25081 hypodermia 1
1027	293	21.3	246	1	Q9R2C8	Q9r2c8 rattus norv	1100	287	20.9	273	2	Q9VEM5	Q9vem5 drosophila
1028	293	21.3	247	1	MCT3_RAT	P50339 rattus norv	1101	287	20.9	268	2	Q8T4T3	Q8t4t3 aedes aegyp
1029	293	21.3	265	1	SER1_DROME	P17205 drosophila	1102	287	20.9	273	2	Q9VEM5	Q9vem5 drosophila
1030	293	21.3	268	2	O16900	Q16900 aedes aegyp	1103	287	20.9	416	2	Q8ET26	Q8et26 homo sapien
1031	293	21.3	268	2	O8N0R8	Q8n0r8 aedes aegyp	1104	287	20.9	422	1	DE51_HUMAN	DE51 human
1032	293	21.3	277	2	Q8VFN8	Q8vfn8 drosophila	1105	287	20.9	423	2	Q6UW31	Q6uw31 homo sapien
1033	293	21.3	277	2	Q8VFN8	Q8vfn8 drosophila	1106	287	20.9	481	2	Q819Z5	Q819z5 hyphantria
1034	293	21.3	301	2	Q8VFN8	Q8vfn8 drosophila	1107	287	20.9	581	2	Q819Z5	Q819z5 hyphantria
1035	293	21.3	427	2	Q7Q602	Q7q602 anopheles g	1108	286.5	20.9	218	1	Q7OM61	Q7om61 anopheles g
1036	293	21.3	433	1	UROK_PAPCY	P16237 papio cynoc	1109	286.5	20.9	220	2	Q7PTP7	Q7ptp7 anopheles g
1037	293	21.3	777	2	Q8CAN9	Q8can9 mus musculu	1110	286.5	20.9	376	2	Q7PTP7	Q7ptp7 anopheles g
1038	293	21.3	855	1	SP1A_MOUSE	S66177 mus musculu	1111	286.5	20.9	425	2	Q7PTP7	Q7ptp7 anopheles g
1039	292.5	21.3	235	2	Q903E7	Q903e7 cynops pyrr	1112	286	20.8	235	2	Q6XGZ4	Q6xgz4 anopheles g
1040	292.5	21.3	236	2	Q921H1	Q921h1 mus musculu	1113	286	20.8	254	1	CTRL_HAURU	CTRL hauru
1041	292.5	21.3	390	2	Q8MP08	Q8mp08 bombyx mori	1114	286	20.8	416	2	Q8B2J3	Q8b2j3 mus musculu
1042	292.5	21.3	469	2	Q9GMD9	Q9gmd9 ornithorhyn	1115	286	20.8	416	2	Q8B2J3	Q8b2j3 mus musculu
1043	292	21.3	257	2	Q8T6J9	Q8t6j9 aedes aegyp	1116	286	20.8	443	2	Q8B2J3	Q8b2j3 mus musculu
1044	292	21.3	268	1	CLCR_RAT	P55031 rattus norv	1117	286	20.8	667	2	Q9BJM1	Q9bjm1 brachydanio
1045	292	21.3	270	2	Q8T4A8	Q8t4a8 drosophila	1118	286	20.8	175	2	Q6PLJ9	Q6plj9 squilla ora
1046	292	21.3	276	2	Q97398	Q97398 phaeton coc	1119	285.5	20.8	248	1	MCT8_RAT	Mct8 rat
1047	292	21.3	332	2	Q8SY58	Q8sy58 drosophila	1120	285.5	20.8	270	1	EL3A_HUMAN	EL3a human
1048	292	21.3	413	2	Q8T9T2	Q8t9t2 aedes aegyp	1121	285.5	20.8	270	2	Q96QL8	Q96ql8 homo sapien
1049	292	21.3	475	2	Q804W9	Q804w9 fuju rubrip	1122	285.5	20.8	270	2	Q96QL8	Q96ql8 homo sapien
1050	292	21.3	688	1	Q868H6	Q868h6 brachyostom	1123	285.5	20.8	289	2	Q910J9	Q910j9 gadus morhu
1051	291.5	21.2	216	1	CTR2_VESOR	P00768 vespa orien	1124	285.5	20.8	289	2	Q8MR67	Q8mr67 drosophila
1052	291.5	21.2	228	2	Q9Z1D3	Q9z1d3 rattus norv	1125	285.5	20.8	290	2	Q9VPT2	Q9vpt2 ciona intes
1053	291.5	21.2	235	2	Q9NBC9	Q9nbc9 glossina mo	1126	285	20.7	470	2	Q8T3A1	Q8t3a1

1127	284.5	20.7	172	2	06T776	06E776	homo sapien	1200	277	20.2	273	2	Q9VKA8	Q9VKA8	drosophila
1128	284.5	20.7	245	1	06DKO3	06dkq3	eisenia foe	1201	277	20.2	398	2	08MKP4	08mkp4	drosophila
1129	284.5	20.7	253	2	CAC3_BOVIN	P05805	bos taurus	1202	277	20.2	1629	2	Q9V513	Q9v513	drosophila
1130	284.5	20.7	564	1	Q7RTZ1	Q7rtz1	homo sapien	1203	277	20.2	1674	2	Q8S135	Q8s135	drosophila
1131	284	20.7	243	2	Q6B4R4	Q6b4r4	bos taurus	1204	276.5	20.1	257	2	Q97099	Q97099	anopheles d
1132	284	20.7	233	2	001309	001309	botryllus s	1205	276.5	20.1	262	2	Q9VSJ2	Q9vsj2	drosophila
1133	284	20.6	257	2	Q86PL8	Q86pl8	aedes aegypt	1206	276	20.1	254	1	PNR3_MOUSE	PNR3	mouse
1134	283.5	20.6	268	2	Q9XYS6	Q9xys6	crenaceophal	1207	276	20.1	257	2	Q81BE4	Q81be4	ochlerotacu
1135	283.5	20.6	707	2	Q8QGV0	Q8qgv0	cyprinus ca	1208	276	20.1	271	1	S24D_ANOGA	S24d	anophles g
1136	283	20.6	247	1	TRYP_SIMVI	P35048	stimulium vi	1209	276	20.1	300	2	Q7Q6T1	Q7q6t1	anophles g
1137	283	20.6	320	2	Q7QKJ3	Q7qk13	anophles g	1210	276	20.1	302	2	Q9VCJ0	Q9vcj0	anophles g
1138	283	20.6	382	2	Q7EHL1	Q7ehl1	mus muscicu	1211	276	20.1	376	1	FA10_HUPST	FA10	hupst
1139	282.5	20.6	245	2	Q7PJ00	Q7pj00	anophles g	1212	276	20.1	488	1	FA10_HUMAN	FA10	human
1140	282.5	20.6	246	2	Q817P0	Q817p0	lumbriacus b	1213	276	20.1	717	2	Q8AXR1	Q8axr1	xenopus lae
1141	282.5	20.6	267	2	Q9VLF5	Q9vlf5	drosophila	1214	275.5	20.1	245	2	Q8C1O8	Q8c1o8	mus muscicu
1142	282.5	20.6	269	2	Q9V929	Q9v929	drosophila	1215	275.5	20.1	249	2	Q8C1O8	Q8c1o8	mus muscicu
1143	282.5	20.6	424	2	Q6R5S8	Q6r5s8	ochlerotacu	1216	275.5	20.1	256	2	Q81B85	Q81b85	ochlerotacu
1144	282.5	20.6	687	2	Q6KRF3	Q6krf3	neodiprion	1217	275.5	20.1	258	2	Q6NLM5	Q6nlm5	drosophila
1145	282	20.5	258	2	Q6KRF3	Q6krf3	neodiprion	1218	275.5	20.1	262	2	Q9V5X9	Q9v5x9	drosophila
1146	282	20.5	259	2	Q18600	Q18600	drosophila	1219	275.5	20.1	296	2	Q8T9U6	Q8t9u6	aedes aegyp
1147	282	20.5	263	2	Q9NB92	Q9nb92	agrotis ips	1220	275	20.0	237	2	Q17035	Q17035	anophles g
1148	282	20.5	416	1	HEPS_RAT	Q05511	rattus norv	1221	275	20.0	256	2	Q25082	Q25082	hypoderma 1
1149	282	20.5	686	1	Q6Q1Q9	Q6q1q9	gallus gall	1222	275	20.0	260	2	Q9VSU1	Q9vsu1	drosophila
1150	282	20.5	688	2	Q868H4	Q868h4	branchiosteo	1223	275	20.0	262	2	Q7Z0G3	Q7z0g3	phlebotomus
1151	281.5	20.5	258	2	Q9NGY6	Q9ngy6	aedes aegyp	1224	275	20.0	284	2	Q8AXO8	Q8axo8	xenopus lae
1152	281.5	20.5	391	2	Q8MLC5	Q8mlc5	drosophila	1225	275	20.0	317	2	Q7Q619	Q7q619	anophles g
1153	281.5	20.5	388	2	Q7Z1F0	Q7z1f0	cotesia rub	1226	275	20.0	496	2	Q8CHP7	Q8chp7	cavia porce
1154	281.5	20.5	430	2	Q7PNQ4	Q7pnq4	anophles g	1227	275	20.0	717	2	Q8AXR0	Q8axr0	xenopus lae
1155	281	20.5	262	2	Q7Z0G5	Q7z0g5	phlebotomus	1228	274.5	20.0	695	1	CASP_MESAU	CASP	mesau
1156	281	20.5	267	2	Q9VA66	Q9va66	drosophila	1229	274	19.9	87	2	Q9VCQ78	Q9vcq78	m mus muscu
1157	281	20.5	564	2	Q8MKR1	Q8mkb1	oryctolagus	1230	274	19.9	265	2	Q9VHF7	Q9vhf7	drosophila
1158	281	20.5	564	2	Q8MKR1	Q8mkb1	oryctolagus	1231	273	19.9	125	2	Q86V18	Q86v18	homo sapien
1159	280.5	20.4	227	2	Q7PBR4	Q7pbr4	anophles g	1232	273	19.9	247	1	MCT8_MOUSE	MCT8	mouse
1160	280.5	20.4	235	2	Q97100	Q97100	anophles g	1233	273	19.9	254	2	Q8K557	Q8k557	rattus norv
1161	280.5	20.4	270	2	Q7Q0N6	Q7q0n6	anophles g	1234	273	19.9	257	2	Q81B83	Q81b83	aedes polyn
1162	280.5	20.4	365	2	Q9Y1K7	Q9y1k7	anophles g	1235	273	19.9	258	1	TRFY_DROBR	TRFY	drobr
1163	280.5	20.4	410	2	Q7QJ44	Q7qj44	anophles g	1236	273	19.9	265	2	Q17800	Q17800	caenorhabdi
1164	280.5	20.4	424	2	Q6R559	Q6r559	ochleria nu	1237	273	19.9	288	2	Q9VEM8	Q9vem8	drosophila
1165	280.5	20.4	439	2	Q8BHM9	Q8bhm9	m mus muscu	1238	273	19.9	377	2	P79343	P79343	bos taurus
1166	280	20.4	241	2	Q7PQB3	Q7pqb3	anophles g	1239	272.5	19.8	258	2	Q9GME1	Q9gme1	ornithorhyn
1167	280	20.4	254	1	TRYP_SARBU	P51588	sarcophaga	1240	272.5	19.8	262	1	TRFY_DROME	TRFY	drome
1168	280	20.4	267	2	Q8SYK8	Q8syk8	drosophila	1241	272.5	19.8	282	2	Q7PXP30	Q7pxp30	anophles g
1169	280	20.4	271	2	Q9V4M5	Q9v4m5	drosophila	1242	272.5	19.8	688	1	CIS_HUMAN	CIS	human
1170	280	20.4	282	2	Q25395	Q25395	lumbriacus r	1243	272.5	19.8	432	1	UBOK_RAT	UBOK	rat
1171	280	20.4	336	2	Q7RTY5	Q7rty5	homo sapien	1244	272.5	19.8	537	2	Q8Q4H8	Q8q4h8	fugu rubrip
1172	280	20.4	420	2	Q61E14	Q61e14	rattus norv	1245	272.5	19.8	978	2	P91777	P91777	pacifastacu
1173	280	20.4	494	2	Q9VJD7	Q9vjdt7	drosophila	1246	272	19.8	243	2	Q01310	Q01310	botryllus s
1174	279.5	20.3	745	2	Q9PVY3	Q9pvv3	cyprinus ca	1247	272	19.8	262	1	TRYT_DROME	TRYT	drome
1175	279	20.3	242	2	Q6T374	Q6t374	eisenia foe	1248	272	19.8	262	2	Q9V5Y0	Q9v5y0	drosophila
1176	279	20.3	248	2	Q9Z0S1	Q9z0s1	mus muscicu	1249	272	19.8	288	1	Q8SK49	Q8sk49	drosophila
1177	279	20.3	267	2	Q9VA67	Q9va67	drosophila	1250	272	19.8	475	1	FA10_CHICK	FA10	chick
1178	279	20.3	280	1	TRYZ_DROME	P42280	drosophila	1251	272	19.8	492	2	Q7Z155	Q7z155	chlitomantes
1179	279	20.3	280	2	Q9V5X8	Q9v5x8	drosophila	1252	272	19.8	688	1	CIS_HUMAN	CIS	human
1180	279	20.3	319	2	Q9VR55	Q9vr55	drosophila	1253	272	19.8	688	2	Q8CFG8	Q8cfg8	homo sapien
1181	279	20.3	329	2	Q9GL10	Q9gl10	ovis aries	1254	271.5	19.8	250	2	Q7PWE3	Q7pwe3	anophles g
1182	279	20.3	385	2	Q25101	Q25101	herdmania m	1255	271.5	19.8	257	2	Q81S83	Q81s83	aedes altop
1183	279	20.3	694	2	Q8R099	Q8r099	mus muscicu	1256	271.5	19.8	262	2	Q9NB91	Q9nb91	agrotis ips
1184	279	20.3	721	2	Q6P6T1	Q6p6t1	rattus norv	1257	271.5	19.8	267	2	Q9V942	Q9v942	drosophila
1185	279	20.3	924	2	Q7ZT69	Q7zt69	lampetra jay	1258	271.5	19.8	272	2	Q9VRS3	Q9vrs3	drosophila
1186	278.5	20.3	326	2	Q7PMT2	Q7pmt2	anophles g	1259	271.5	19.8	833	2	Q96442	Q96442	strongyloce
1187	278.5	20.3	326	2	Q7Z280	Q7z280	brachydanio	1260	271	19.7	247	2	Q70164	Q70164	mesocricetu
1188	278.5	20.3	330	2	Q61BE2	Q61be2	rattus norv	1261	271	19.7	253	2	Q9XY50	Q9xy50	crenaceophal
1189	278.5	20.3	593	1	FA12_BOVIN	P96140	bos taurus	1262	271	19.7	275	2	Q7Z084	Q7z084	stomoxys ca
1190	278	20.2	239	2	Q9NKC5	Q9nkc5	drosophila	1263	271	19.7	1801	2	Q8WSJ2	Q8wsj2	bombyx mori
1191	278	20.2	474	2	Q7PZH7	Q7pzh7	anophles g	1264	270.5	19.7	219	2	Q7PJ75	Q7pj75	anophles g
1192	278	20.2	490	1	FA10_RABIT	Q13905	oryctolagus	1265	270.5	19.7	245	2	Q61E56	Q61e56	rattus norv
1193	278	20.2	501	2	Q7QCV0	Q7qcvo	anophles g	1266	270.5	19.7	248	1	GRAD_MOUSE	GRAD	mouse
1194	277.5	20.2	245	2	Q9BLT8	Q9blt8	lumbriacus r	1267	270.5	19.7	256	1	TRYP_MANSE	TRYP	manse
1195	277.5	20.2	266	2	Q24091	Q24091	drosophila	1268	270.5	19.7	420	2	Q7Q235	Q7q235	anophles g
1196	277.5	20.2	845	2	Q9G519	Q9g519	stomoxys ca	1269	270	19.7	253	2	Q18440	Q18440	hellioverpa
1197	277.5	20.2	845	2	Q9DGRI	Q9dgr1	xenopus lae	1270	270	19.7	297	2	Q7Q604	Q7q604	anophles g
1198	277	20.2	252	2	Q76498	Q76498	diaprepes a	1271	270	19.7	694	2	Q70542	Q70542	rattus norv
1199	277	20.2	272	2	Q82KGO	Q82kgo	streptomyce	1272	269.5	19.6	248	1	GR22_RAT	GR22	rat

1273	269.5	19.6	339	2	06BDAB	06bd8	penaeus	jap	1346	262	19.1	266	2	09VMX7	09vmx7	drosoophila
1274	269	19.6	235	2	09GTX7	09gtx7	aedes	albop	1347	262	19.1	272	2	08SZG4	08szg4	drosoophila
1275	269	19.6	244	2	08MWS	08mws	dermatophag		1348	262	19.1	290	2	07PVQ3	07pvq3	anopheles
1276	269	19.6	375	2	09NMS8	09nae8	anopheles	g	1349	262	19.1	427	2	07Q6T1	07q6t1	anopheles
1277	269	19.6	389	2	07QGN4	07qgn4	anopheles	g	1350	262	19.1	504	2	06GWT7	06gwt7	brachydanio
1278	269	19.6	445	2	07Q9S6	07q9s6	anopheles	g	1351	261.5	19.0	259	2	04S048	04s048	anopheles
1279	269	19.6	2616	1	NDL DROME	p9815	drosoophila	g	1352	261.5	19.0	259	2	07PX38	07px38	anopheles
1280	268.5	19.5	245	2	06DF10	06df10	xenopus	cto	1353	261.5	19.0	297	2	07QNM1	07qnm1	anopheles
1281	268.5	19.5	256	2	09Y442	09y442	metarhizium		1354	261.5	19.0	324	2	06BD08	06bd08	anopheles
1282	268.5	19.5	260	2	07Z0G4	07z0g4	phlebotomus		1355	261.5	19.0	366	2	07Q170	07q170	mus musculus
1283	268.5	19.5	261	2	000344	000344	cochliobolu		1356	261.5	19.0	421	1	ACRO_HUMAN	p10332	homo sapien
1284	268.5	19.5	262	1	TRYT DROER	066d0	culicoides		1357	261.5	19.0	669	2	07PWE1	07pwe1	anopheles
1285	268.5	19.5	275	2	070W31	070w31	oncorhynch		1358	261	19.0	239	2	07P595	07p595	rattus norv
1286	268.5	19.5	707	2	06PLJ6	p24158	homo sapien		1360	261	19.0	262	2	07QFW4	07qfw4	anopheles
1287	268	19.5	256	1	PRN3_HUMAN	09vka9	branchiosto		1361	261	19.0	316	2	09VAG2	09vag2	drosoophila
1288	268	19.5	270	2	09VKA9	06p1j5	penaeus	jap	1362	260.5	19.0	242	1	FIBC_LUDRU	p8328	lumbircus r
1290	268	19.5	277	2	06M60	06m60	branchiosto		1363	260.5	19.0	242	2	0966B7	0966b7	lumbircus r
1291	267.5	19.5	249	2	06IB63	06ib63	rattus norv		1364	260.5	19.0	242	2	08MX72	08mx72	eisenia b
1292	267.5	19.5	255	2	044332	06p1j5	neocardiina		1365	260.5	19.0	242	2	06T373	06t373	eisenia foe
1293	267.5	19.5	280	2	06GLK1	06glk1	xenopus	lae	1366	260.5	19.0	245	2	07PFP6	07pfp6	anopheles
1294	267	19.4	182	2	06PLJ5	08szq7	drosoophila		1367	260.5	19.0	264	2	09VT25	09vt25	drosoophila
1295	267	19.4	252	2	08SZQ7	08szq7	drosoophila		1368	260.5	19.0	298	2	07PZ90	07p290	drosoophila
1296	267	19.4	271	2	07PIA2	07pia2	anopheles	g	1369	260.5	19.0	688	2	09PVY4	09pv4	anopheles
1297	267	19.4	388	2	08I926	08i926	hyphantria		1370	260	18.9	257	2	08IBE2	08ibe2	aedes trise
1298	266	19.4	222	2	07SIG2	07sig2	solenopsis		1371	260	18.9	252	2	07PVP7	07pvp7	anopheles
1299	266	19.4	252	1	TRV1 DROME	p52905	drosoophila		1372	260	18.9	302	2	08II9G	08ii9g	drosoophila
1300	266	19.4	254	2	09XYX0	09xyx0	rhizophertia		1373	259.5	18.9	252	2	06I388	06i388	mus musculu
1301	266	19.4	266	2	09YEM9	09yem9	drosoophila		1374	259.5	18.9	275	2	06HUC4	06huc4	mus musculu
1302	266	19.4	273	2	08MTU7	08mtu7	drosoophila		1375	259.5	18.9	309	2	06DHU4	06dhu4	brachydanio
1303	266	19.4	277	2	08MLC4	08mlc4	drosoophila		1376	259.5	18.9	324	2	06BD05	06bd05	drosoophila
1304	266	19.4	400	2	09GRG2	09grg2	tenebrio	mo	1377	259.5	18.9	334	2	06BD06	06bd06	drosoophila
1305	265	19.3	506	2	07PR64	07pr64	anopheles	g	1378	259.5	18.9	344	2	06BD16	06bd16	drosoophila
1306	265.5	19.3	322	2	06BD03	06bd03	drosoophila		1379	259.5	18.9	511	2	09VZHS	09vzhs	drosoophila
1307	265.5	19.3	434	2	09VTS7	09vts7	drosoophila		1380	259.5	18.9	546	2	08SXG6	08sxg6	drosoophila
1308	265.5	19.3	444	2	09V4W6	09v4w6	drosoophila		1381	259	18.9	248	1	GRAE_MOUSE	p08884	mus musculu
1309	265	19.3	251	2	09VQ99	09vq99	drosoophila		1382	259	18.9	263	2	09V5X7	09v5x7	drosoophila
1310	265	19.3	277	2	07QKX3	07qkx3	anopheles	g	1383	259	18.9	279	2	07OE41	07oe41	anopheles
1311	265	19.3	322	2	098G16	098g16	rhizobium	l	1384	258.5	18.8	167	2	06URK3	06urk3	bochtrups ja
1312	265	19.3	415	1	ACRO_PIG	p08001	sus scrofa		1385	258.5	18.8	248	2	06IBS8	06ibs8	rattus norv
1313	265	19.3	415	1	029015	029015	sus sp.	pre	1386	258.5	18.8	285	2	069997	069997	strectomyce
1314	264.5	19.3	247	2	07PFP5	07pfp5	anopheles	g	1387	258.5	18.8	459	2	09V4W7	09v4w7	drosoophila
1315	264.5	19.3	248	1	TRV1_NANSE	p35045	manduca	sex	1388	258.5	18.8	522	2	08MQM9	08mqm9	drosoophila
1316	264.5	19.3	256	1	TRV1_NANSE	007943	bombyx	mori	1389	258.5	18.8	1089	2	08T3A0	08t3a0	ciona
1317	264.5	19.3	264	1	VDP_BOWMO	066663	callinectes		1390	258	18.8	267	2	09GP27	09gp27	drosoophila
1318	264.5	19.3	369	2	0606S3	0606s3	triakis	scy	1391	258	18.8	269	2	07Q515	07q515	anopheles
1319	264.5	19.3	719	2	09PVY2	09pv2	homo sapien		1392	258	18.8	277	2	07PG95	07pg95	anopheles
1320	264	19.2	176	2	015098	p20160	homo sapien		1393	258	18.8	295	2	018445	018445	hellicoverpa
1321	264	19.2	180	2	096A30	096a30	homo sapien		1394	258	18.8	300	2	07Q6U0	07q6u0	anopheles
1322	264	19.2	301	2	07PKG5	07pkg5	drosoophila		1395	258	18.8	352	2	07KVM3	07kvm3	drosoophila
1323	263.5	19.2	251	1	CAP7_HUMAN	015098	homo sapien		1396	257.5	18.7	196	2	06VFC8	06vfc8	anopheles
1324	263.5	19.2	256	2	06R561	06r561	anopheles	g	1397	257.5	18.7	248	2	06IEB9	06ieb9	rattus norv
1325	263.5	19.2	258	2	09VMX9	09vmx9	drosoophila		1398	257.5	18.7	254	2	001136	001136	metarhizium
1326	263.5	19.2	421	1	TRVZ DROER	p54630	drosoophila		1399	257.5	18.7	248	2	097098	097098	anopheles
1327	263.5	19.2	180	2	06TKC2	06tkc2	homo sapien		1400	257.5	18.7	254	2	0961Y0	0961y0	galleria me
1328	263	19.1	241	2	06T775	06t775	homo sapien		1401	257.5	18.7	255	2	097097	097097	anopheles
1329	263	19.1	248	2	07Q5E4	07q5e4	anopheles	g	1402	257.5	18.7	274	2	06DHC9	06dhc9	anopheles
1330	263	19.1	257	2	09VZT0	09vzt0	drosoophila		1403	257.5	18.7	286	2	096900	096900	brachydanio
1331	263	19.1	257	2	07QIHS	07qihs	anopheles	g	1404	257.5	18.7	326	2	07RTY6	07rty6	homo sapien
1332	263	19.1	289	2	0945T9	0945t9	anopheles	g	1405	257.5	18.7	236	2	06LBN2	06lbn2	homo sapien
1333	263	19.1	289	2	09N6C6	09n6c6	phytophor		1406	257	18.7	256	2	018441	018441	homo sapien
1334	263	19.1	295	2	09N6C6	09n6c6	heliolithis	z	1407	257	18.7	284	2	08MLV8	08mlv8	helicoverpa
1335	263	19.1	405	2	08IN70	08in70	drosoophila		1408	257	18.7	284	2	06JEB0	06jeb0	homo sapien
1336	263	19.1	405	2	08SZG0	08szg0	pseudonaja		1409	256.5	18.7	196	2	06VFP0	06vfp0	homo sapien
1337	263	19.1	467	2	06IT09	06it09	pseudonaja		1410	256.5	18.7	235	1	TRVZ_HUMAN	06bzj3	homo sapien
1338	262.5	19.1	256	1	TRVY MANSE	p35047	manduca	sex	1411	256.5	18.7	242	2	06NTB8	06ntb8	homo sapien
1339	262.5	19.1	271	2	09VRS6	09vrs6	drosoophila		1412	256.5	18.7	464	2	09NK82	09nk82	drosoophila
1340	262.5	19.1	281	2	08SYB5	08syb5	drosoophila		1413	256.5	18.7	245	2	09XY47	09xy47	ctenocephal
1341	262.5	19.1	433	2	09QWZ2	09qwz2	rattus	sp.	1414	256	18.6	265	2	09XY55	09xy55	ctenocephal
1342	262.5	19.1	778	2	09CVU2	09cvu2	mus musculu		1415	256	18.6	267	2	09VRU0	09vr0	drosoophila
1343	262	19.1	108	2	06PLU7	06plu7	femneropena		1416	256	18.6	282	2	07OCX2	07ocx2	anopheles
1344	262	19.1	183	2	09VQ97	09vq97	drosoophila		1417	256	18.6	403	2	09KSQ6	09ksq6	vibrio chol
1345	262	19.1	245	2					1418	256	18.6					

1419	256	18.6	421	2	06ZMR5	06zmr5 homo sapien
1420	256	18.6	463	2	06IT10	06it10 pseudonaja
1421	255.5	18.6	220	2	06X143	06x143 drosophila
1422	255.5	18.6	254	2	018436	018436 helicoverpa
1423	255.5	18.6	273	2	07Z163	07z163 dermatophag
1424	255.5	18.6	431	2	07PV05	07pv05 anopheles g
1425	255	18.6	292	2	07PV05	07pv05 anopheles g
1426	255	18.6	405	2	07PN03	07pn03 anopheles g
1427	254.5	18.5	254	2	018434	018434 helicoverpa
1428	254.5	18.5	278	2	P91893	P91893 arenicola m
1429	254.5	18.5	357	2	07Q092	07q092 anopheles g
1430	254.5	18.5	357	2	07QXK6	07qkx6 anopheles g
1431	254.5	18.5	493	2	07PVE2	07pve2 anopheles g
1432	254.5	18.5	524	2	09V819	09v819 drosophila
1433	254.5	18.5	524	2	06MR00	06mr00 drosophila
1434	254.5	18.5	827	2	07PZ88	07pze8 anopheles g
1435	254	18.5	334	2	06BD11	06bd11 drosophila
1436	254	18.5	334	2	09VEA0	09vea0 drosophila
1437	253.5	18.4	282	2	0641D4	0641d4 anthomomus
1438	253	18.4	242	2	09XY59	09xy59 ctenocephal
1439	253	18.4	251	2	09VXC9	09vxc9 drosophila
1440	253	18.4	253	2	09VXC9	09vxc9 drosophila
1441	253	18.4	272	1	06W741	06w741 pediculus h
1442	253	18.4	287	2	0675S0	0675s0 olkopleura
1443	252.5	18.4	245	2	07Q208	07q208 anopheles g
1444	252.5	18.4	254	2	076954	076954 laccanobia c
1445	252.5	18.4	262	2	08MD01	08md01 canis fam11
1446	252.5	18.4	324	2	06BD09	06bd09 drosophila
1447	252	18.3	235	2	07PRK6	07prk6 anopheles g
1448	252	18.3	295	2	018450	018450 helicoverpa
1449	252	18.3	301	2	07Q6T0	07q6t0 anopheles g
1450	252	18.3	400	2	027081	027081 tachyplesus
1451	251.5	18.3	186	2	06X655	06x655 marmota mon
1452	251.5	18.3	266	2	08MLC2	08mlc2 drosophila
1453	251.5	18.3	267	2	09VGB8	09vgb8 drosophila
1454	251.5	18.3	276	2	018443	018443 helicoverpa
1455	251.5	18.3	318	2	07QC37	07qc37 anopheles g
1456	251.5	18.3	418	2	07Q529	07q529 anopheles g
1457	251.5	18.3	520	2	08ING0	08ing0 drosophila
1458	251	18.3	285	2	07Q5K4	07q5k4 anopheles g
1459	251	18.3	405	2	08MOG8	08mog8 apis mellif
1460	250.5	18.2	226	2	06XHU4	06xhu4 drosophila
1461	250.5	18.2	240	2	07PV11	07pv11 anopheles g
1462	250.5	18.2	268	2	09VT24	09vt24 drosophila
1463	250.5	18.2	305	2	08MR12	08mr12 drosophila
1464	250.5	18.2	323	2	076920	076920 drosophila
1465	250	18.2	124	2	08CG65	08cg65 mus musculu
1466	250	18.2	203	2	09NB77	09nb77 heliothis z
1467	250	18.2	258	2	09V866	09v866 drosophila
1468	250	18.2	274	2	08MUC0	08muc0 glosina fu
1469	249.5	18.2	253	2	018442	018442 helicoverpa
1470	249.5	18.2	254	2	018447	018447 helicoverpa
1471	249.5	18.2	258	2	07Q2P0	07q2p0 anopheles g
1472	249.5	18.2	258	2	07PM15	07pml5 anopheles g
1473	249.5	18.2	274	2	09V8S7	09v8s7 drosophila
1474	249.5	18.2	282	2	018655	018655 plodia inte
1475	249.5	18.2	327	2	08MS77	08ms77 drosophila
1476	249.5	18.2	362	2	06LU71	06lu71 photobacter
1477	249.5	18.2	520	2	08SY93	08sy93 drosophila
1478	249	18.1	253	2	09NGY5	09ngy5 heliothis v
1479	249	18.1	305	2	07Q6S4	07q6s4 anopheles g
1480	249	18.1	388	2	0966V2	0966v2 halocynthia
1481	249	18.1	714	2	07PWE5	07pwe5 anopheles g
1482	248.5	18.1	296	2	091711	091711 drosophila
1483	248.5	18.1	381	2	08MOY4	08moy4 drosophila
1484	248.5	18.1	746	2	001654	001654 halocynthia
1485	248	18.0	141	2	06GKZ6	06gkz6 drosocelia
1486	248	18.0	257	2	08IT49	08it49 pyrococelia
1487	248	18.0	257	2	0945U0	0945u0 phytochlor
1488	248	18.0	258	2	09VZ59	09vz59 drosophila
1489	248	18.0	277	2	07QL41	07ql41 anopheles g
1490	248	18.0	277	2	07QNM2	07qnm2 anopheles g
1491	248	18.0	367	2	070169	070169 mus musculu

1492	248	18.0	374	2	080YD5	080yd5 mus musculu
1493	248	18.0	392	2	09VMZ3	09vmz3 drosophila
1494	248	18.0	401	2	06LH17	06lh17 photobacter
1495	247.5	18.0	260	2	09U414	09u414 plodia inte
1496	247.5	18.0	291	2	06Y1Y9	06y1y9 lygus lineo
1497	247	18.0	243	2	07M413	07m413 megabombus
1498	247	18.0	278	2	07Q805	07q805 anopheles g
1499	247	18.0	350	2	09VC09	09vc09 drosophila
1500	247	18.0	360	2	09W1X6	09w1x6 drosophila
ALIGNMENTS						
RESULT 1						
KXKC_HUMAN						
ID	KXKC_HUMAN	STANDARD;	PRT;	248	AA.	
AC	Q9UKR0; Q9UKR1;					
DT	16-OCT-2001 (Rel. 40, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DT	25-OCT-2004 (Rel. 45, Last annotation update)					
DE	Kalikrein 12 precursor (EC 3.4.21.-) (Kalikrein-like protein 5)					
DE	(KXKC-L5) (UNQ669/PRO1303).					
GN	Name=KXKC12; Synonyms=KXKC15;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A. (ISOFORM 1).					
RX	MEDLINE=20118156; PubMed=10652563;					
RA	Yousef G.M., Luo L.-Y., Diamandis E.P.;					
RT	"Identification of novel human kalikrein-like genes on chromosome					
RT	19q13.3-q13.4.";					
RL	Anticancer Res. 19:2843-2852(1999).					
RN	[2]					
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).					
RA	Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;					
RT	"Cloning of new alternatively spliced forms of the kalikrein-like					
RT	gene 5 (KXKC-L5).";					
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.					
RN	[3]					
RP	SEQUENCE FROM N.A. (ISOFORM 1).					
RX	PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;					
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,					
RA	Moss P., Paepker B., Wang K.;					
RT	"Sequencing and expression analysis of the serine protease gene					
RT	cluster located in chromosome 19q13 region.";					
RL	Gene 257:119-130(2000).					
RN	[4]					
RP	SEQUENCE FROM N.A. (ISOFORM 1).					
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,					
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,					
RA	Barton D., Foster J., Grimaldi C., Gu O., Hass P.E., Helens S.,					
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,					
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,					
RA	Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagte A.,					
RA	Vanclan R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yanesa D.,					
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,					
RA	Godowski P., Gray A.;					
RT	"The secreted protein discovery initiative (SPDI), a large-scale					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment.";					
RL	Genome Res. 13:2265-2270(2003).					
RN	[5]					
RP	SEQUENCE FROM N.A.					
RX	PubMed=15057824; DOI=10.1038/nature02399;					
RA	Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,					
RA	Lameterin J.E., Hellsten U., Goodstein D., Coutume O., Tran-Gyamfi M.,					
RA	Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,					
RA	Canenevel S., Carrano A.V., Caolile C., Chan Y.M., Christensen M.,					
RA	Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,					

RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
 RA Glavina T., Gomez M., Gonzales E., Groza M., Hamon N., Hawkins T.,
 RA Haydu L., Ho I., Huang W., Israeli S., Jett J., Kadner K., Kimball H.,
 RA Kikayishi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
 RA Malfaceti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
 RA Nelson K., Nolan M., Ovcharenko I., Pfluck S., Pollard M.,
 RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
 RA Rodriguez A., Rogers S., Salamo A., Salazar A., She X., Smith D.,
 RA Slezak T., Solovoy V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
 RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
 RA Furey T.S., DeLong P., Dickson M., Gordon D., Eichler E.E.,
 RA Penacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
 RA Rubin E.M., Lucas S.M.,
 RA "The DNA sequence and biology of human chromosome 19."
 RL Nature 428:529-535(2004).
 CC -1 SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1 ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9UKR0-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9UKR0-2; Sequence=VSP_005403;
 CC -1 SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF135025; AAD26426.2; -;
 DR EMBL; AF135025; AAF06065.1; -;
 DR EMBL; AE243527; AAG33365.1; -;
 DR EMBL; AY358524; AAO88888.1; -;
 DR EMBL; AC011473; AAG23258.1; -;
 DR HSSP; P00760; IEZX.
 DR MEROPS; S01.020; -;
 DR Genew; HGNC:6360; KLK12.
 DR MIM; 605539; -;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0004252; P:serine-type endopeptidase activity; NAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001354; Peptidase_S1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PSS0240; TRYP_SIN_DOM; 1.
 DR PROSITE; PSS0134; TRYP_SIN_HIS; 1.
 DR PROSITE; PSS0135; TRYP_SIN_SER; 1.
 KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
 KW signal.
 FT SIGNAL 1 17 potential.
 FT CHAIN 18 248 Kallikrein 12.
 FT ACT_SITE 62 62 Charge relay system (By similarity).
 FT ACT_SITE 108 108 Charge relay system (By similarity).
 FT ACT_SITE 200 200 Charge relay system (By similarity).
 FT DISULFID 28 161 By similarity.
 FT DISULFID 47 63 By similarity.
 FT DISULFID 133 235 By similarity.
 FT DISULFID 140 206 By similarity.
 FT DISULFID 172 186 By similarity.
 FT DISULFID 196 222 By similarity.
 FT CARBOHYD 24 24 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 163 163 KYVDWIRIMIRRN -> NSTLVGLGTSKMNFSQCP (in
 FT VARSPLIC 236 248 isoform 2).
 FT SEQUENCE 248 AA; 26733 MW; BB473B98FB8AF703 CRC64;

Query Match 100.0%; Score 1374; DB 1; Length 248;
 Best local similarity 100.0%; Pred. NO. 3.5e-102;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSLFLLCVLGLSQATPKIFNGTECGRNSQPMQVLEFGTSILRCGYLIDHRWLTA 60
 DB 1 MGSLFLLCVLGLSQATPKIFNGTECGRNSQPMQVLEFGTSILRCGYLIDHRWLTA 60
 QY 61 AHGSGRWVWLGHSLSQLDPMTEQIRHSGFSYTHPGYLGASTSHEDLRLRLPVRV 120
 DB 61 AHGSGRWVWLGHSLSQLDPMTEQIRHSGFSYTHPGYLGASTSHEDLRLRLPVRV 120
 QY 121 TSSVQPLPLPNDCACTAGTECHVSGWGITNHPNPPDLLOCLNLSIYSHATCGVPGRI 180
 DB 121 TSSVQPLPLPNDCACTAGTECHVSGWGITNHPNPPDLLOCLNLSIYSHATCGVPGRI 180
 QY 181 TSNWVACGVPQDACCQDGGGFLVCGGVTCGLVSGSVGPCQDGI PGVYTYICKYVDW 240
 DB 181 TSNWVACGVPQDACCQDGGGFLVCGGVTCGLVSGSVGPCQDGI PGVYTYICKYVDW 240
 QY 241 IRMIRRN 248
 DB 241 IRMIRRN 248
 Db 241 IRMIRRN 248
 RESULT 2
 ID Q9CV76 PRELIMINARY; PRT; 234 AA.
 AC Q9CV76;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched
 DE library, clone:231008B01 product:similar to KALLIKREIN 12 (EC
 DE 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) (Fragment).
 GN Name=KLK12;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carinci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RA The PANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=110756861; DOI=10.1101/gr.152600;
RA Shiba K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama Y., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasahigashi K.,
RA Fujimake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN Integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multiplexed capillary sequencer.";
RM Genome Res. 10:1757-1771(2000).
[6]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Tongue;
RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numasaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shiba K., Shiba Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Taniguchi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL: AK009217; BAB26143.1; -.
DR HESP: P00760; IEXX.
DR MEROPS: S01.020; -.
DR MED: MG1:1916761; K1k12.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR Pfam: PF00089; Trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SMO0020; Tryp_Spc_1.
DR PROSITE: PS50240; TRYPSIN_DOM_1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER_1.
KM Hydrolyase; Protease; Serine protease.
FT NON TER 1
SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD9110 CRC64;
Query Match 69.3%; Score 952.5; DB 2; Length 234;
Best Local Similarity 70.6%; Pred. No. 1.9e-68;
Matches 166; Conservative 27; Mismatches 41; Indels 1; Gaps 1;
QY LSQATPKEFGTCGRNSQPMQVGLFEFTSLRCGGVLDHRRWLLTAHSGSRWVWG 73
Db 1 LSQADREKTINGVECVKNSQPMQVGLFEFTSLRCGGVLDHRRWLLTAHSGSRWVWG 59
QY EHSLSQDLWTQRIHSGFVTHPGYLGASTSHEDLLRLRLPRVTSVQPLPNDG 133
Db 74 EHSLSQDLWTQRIHSGFVTHPGYLGASTSHEDLLRLRLPRVTSVQPLPNDG 133
QY EHSLSQDLWTQRIHSGFVTHPGYLGASTSHEDLLRLRLPRVTSVQPLPNDG 133
Db 60 EHSLSQDLWTQRIHSGFVTHPGYLGASTSHEDLLRLRLPRVTSVQPLPNDG 133
QY 134 ATATGTCGVSGWGTITNHRNPPDLQCLNLSYSHATCGVYRGRITSNMVCAGGVGQ 193
Db 120 VTTAMCHVSGWGTITNHRNPPDLQCLNLSYSHATCGVYRGRITSNMVCAGGVGQ 193
QY 194 DACGDSGGLVCGVLOGLVSMGSGVGPQGDGIPGVVTVYCKYVDYRMIMRN 248
Db 180 DACGDSGGLVCGVLOGLVSMGSGVGPQGDGIPGVVTVYCKYVDYRMIMRN 248
RESULT 3
KLK8_HUMAN

ID KLK8_HUMAN STANDARD; PRT; 260 AA.
AC 060259; O9HC3; O9U19; O9U047;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurotensin precursor (EC 3.4.21.-) (NP) (Kalikrein 8) (Ovasin) (Serine
DE protease TADG-14) (Tumor-associated differentially expressed gene-14
DE protein) (UNQ283/PRO322).
GN Name=KLK8; Synonyms=NRPN, PRSS19, TADG14;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Hippocampus;
RC MEDLINE=96372070; PubMed=9714609; DOI=10.1016/S0378-1119(98)00232-7;
RX Yoshida S., Taniguchi M., Hiraoka A., Shiosaka S.;
RT "Sequence analysis and expression of human neuropilin CDNA and gene.";
RL Gene 213:9-16(1998).
[2]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE=Brain;
RC MEDLINE=99203457; PubMed=10102990;
RX Mitsui S., Teurloka N., Yamashiro K., Nakazato H., Yamaguchi N.;
RT "A novel form of human neuropilin, a brain-related serine protease, is
RT generated by alternative splicing and is expressed preferentially in
RT human adult brain.";
RL Eur. J. Biochem. 260:627-634(1999).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Ovary;
RC MEDLINE=99413504; PubMed=10465494;
RX Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
RA O'Brien T.J.;
RT "Cloning of tumor-associated differentially expressed gene-14, a novel
RT serine protease overexpressed by ovarian carcinoma.";
RL Cancer Res. 59:4435-4439(1999).
[4]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP Gan L., Gellinas R., Gown A.M., Moss P., Smith R., Wang K.;
RA "Molecular cloning and characterization of a novel serine protease,
RT ovasin, a potential molecular marker for ovarian carcinomas.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RX Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepker B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
[6]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Bacon D., Foster J., Grimaldi C., Gu Q., Hase P.E., Helens S.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seebastri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A.,
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yamasu D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[7]
RN SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
RP Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stiliwgen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnea J.,

RA Dangnan L., Erlar A., Christensen M., Georgescu A., Ayila J., Liu S.,
 RA Andrese T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Dharie S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.,
 RT "Sequence analysis of chromosome 19q13.4,"
 RU Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 CC hippocampal plasticity.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O60259-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O60259-2; Sequence=VSP_005401.
 CC -1- TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the
 CC pancreas while isoform 2 is expressed in adult brain and
 CC hippocampus. Both forms are also found in fetal brain and
 CC placenta. Not detected in kidney, spleen, liver and lung.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. kallikrein
 CC subfamily.
 CC -----
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 CC -----
 DR EMBL, AB009849; BAA28673.1; -
 DR EMBL, AB012761; BAA28676.1; -
 DR EMBL, AB010780; BAA88684.1; -
 DR EMBL, AB008390; BAA82665.1; -
 DR EMBL, AB008927; BAA82666.1; -
 DR EMBL, AF055982; AAD56050.1; -
 DR EMBL, AF095742; AAD25979.1; -
 DR EMBL, AF095743; AAD29574.1; -
 DR EMBL, AF243527; AAG33361.1; -
 DR EMBL, AY559036; AAG89395.1; -
 DR EMBL, AC011473; AAG23254.1; -
 DR HSSP, P00760; 1EXX.
 DR MEROPS, S01.244; -
 DR GeneW, HGNC:6369; KLC8.
 DR MIM, 605644; -
 DR GO, GO:0008236; F:serine-type peptidase activity; TAS.
 DR GO, GO:0007399; P:neurogenesis; TAS.
 DR InterPro, IPR009003; Pept_Ser_Cys.
 DR InterPro, IPR001254; Peptidase_S1.
 DR InterPro, IPR001314; Peptidase_S1A.
 DR Pfam, PF000089; Trypsin_1.
 DR PRINTS, PR00722; CHYMOTRYPSIN.
 DR PROSITE, PS00240; TRYPSIN_DOM. 1.
 DR PROSITE, PS00134; TRYPSIN_HIS. 1.
 DR PROSITE, PS00135; TRYPSIN_SER. 1.
 KM Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
 KM Signal; Zymogen.
 FT SIGNAL 1 28 Potential.
 FT PROPEP 29 32 By similarity.
 FT CHAIN 33 260 Neutropin.
 FT ACT_SITE 73 73 Charge relay system (By similarity).
 FT ACT_SITE 120 120 Charge relay system (By similarity).
 FT ACT_SITE 212 212 Charge relay system (By similarity).
 FT DISULFID 39 173 By similarity.
 FT DISULFID 58 74 By similarity.
 FT DISULFID 145 246 By similarity.
 FT DISULFID 152 218 By similarity.
 FT DISULFID 184 198 By similarity.
 FT DISULFID 208 233 By similarity.
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 23 23 A -> AACGSLDLITKLYANLPCVHLNPNQWPSQPSHCRCG

FT FT WRSNPLPPAA (in isoform 2).
 FT /FTID=VSP_005401.
 SQ SEQUENCE 260 AA; 28048 MW; EF439E5B8C3B660 CRC64;
 Query Match 45.9%; Score 630.5; DB 1; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.3e-42;
 Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;
 QY 5 FELL-----CVLSQAATPKIFNGTECGRNSQPMVQGLFEGTSLRCGVLIDIRWYLTAA 61
 DB 13 MFLLLLGAMAGHSRAQEDKVLGGHBEQPHSQWQALFPGQQLLCGVVLGVGNWUTAA 72
 QY 62 HCSSSRKRWVVLGHSLSQLDWTQIRHSGSVTHPGYLGAST-SHEHDLRLRLRPVRY 120
 DB 73 HCKKPKYTVRLGHSILQNKDQPEQIIPVVSIPHPPCNSDVEDNHNHDLMLQLRDAQSL 132
 QY 121 TSSVQPLPLPNDCAATAGTECHVSGWGTTHPRNPFDLLQCLNLSTVSHATCGVYRGR 180
 DB 133 GSKTKPISLDHCTQPGQKCTVSGMGTVSPRENFPDITLANCAEVKIFPQKCEDAVPGOI 192
 QY 181 TSNMVCAGVPGQDACQGSGBPLVCGVGLGVLSVSGVPGCGDGIPEGVYICKRYDW 240
 DB 193 TDGWCACGSSSKGADTCQGSGBPLVCDGALQGITWSG-DPCGRSDKPEGVYTNICKYLDW 251
 QY 241 IBMIM 245
 DB 252 IKKII 256
 RESULT 4
 08IW69 PRELIMINARY; PRT; 260 AA.
 AC 08IW69;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
 DE Kallikrein 8, isoform 1 preproprotein.
 GN Name=KLC8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences,"
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RU Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL, BC040887; AAB40887.1; -

Query	Match	Similarity	Score	DB 2	Length	260
DR	HSBP; P00760; 1EXZ.		45.7%			
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.					
DR	GO; GO:0008233; F:peptidase activity; IEA.					
DR	GO; GO:0004295; F:trypsin activity; IEA.					
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.					
DR	InterPro; IPR001254; Peptidase SL.					
DR	InterPro; IPR001314; Peptidase SLA.					
DR	InterPro; IPR009003; Pept_Ser_Cys.					
DR	Pfam; PF00089; Trypsin_1.					
DR	PRINTS; PR00722; CHYMOTRYPSIN.					
DR	SMART; SM00020; Tryp_SPC; 1.					
DR	PROSITE; PS00240; TRYPsin DOM; 1.					
DR	PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.					
DR	PROSITE; PS00135; TRYPsin_SER; 1.					
KW	Hydrolase; Protease; Serine protease.					
SW	SEQUENCE 260 AA; 28090 MW; EF5934AB96295660 CRC64;					
Query Match		45.7%;	Score 627.5;	DB 2;	Length 260;	
Best Local Similarity		50.2%;	Pred. No. 2.2e-42;			
Matches 123;	Conservative 24;	Mismatches 93;	Indels 5;	Gaps 3		
QY	5 IFLLL---CVLGLSQATPKIFNGTECCRNSSQPMQVGFEGTSLRCGVLIDHRWLTAA 61					
DB	13 MFLLLGGAMKCHSQAQEDKVLGHECCQPHSPWQALFPGQQLCCGVLVGGNNVLTAA 72					
QY	62 HCSGRYVWRLGEHSLSQLDWTEQIRHSGFSVTHPGYLCAST-SHEHDLRLRLPYRV 120					
DB	73 HCKRKYTVRLGDHSLQNKDGEQEI PVQGSIPHCYNSDVEDNHDMLQLDQASL 132					
QY	121 TTSVQPLPLPNDCAATGTECHVSGMGITNHPNPFPDLCLNLISVSHATCHGYPPRI 180					
DB	133 GSKVPEISLAHCTCPQPGKCTVSGGVTSPRENPPTLNCLEVKI POKKEDAYPQOI 192					
QY	181 TSNWACAGVPGQDACQGSGLPGVLCGLVSMGSGVPGCGDIPGVYTYCKYDWM 240					
DB	193 TDVWVCAAGSSKQADTCQGDSSGPLYCDALQGITSMGS-DPCGRDKEGVYTNICRYIDW 251					
QY	241 IRMTM 245					
DB	252 IKKII 256					
RESULT 5						
NRPN_MOUSE	STANDARD;	PRT;	260 AA.			
ID	NRPN_MOUSE					
AC	061955;					
DT	15-JUL-1999 (Rel. 38, Created)					
DT	15-JUL-1999 (Rel. 38, Last sequence update)					
DT	25-OCT-2004 (Rel. 45, Last annotation update)					
DE	Neutropin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).					
GN	Name=KlK8; Synonyms=Nrpn, Prs619;					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=BALB/C; TISSUE=Hippocampus;					
FX	MEDLINE=95348017; Pubmed=7623137;					
RA	Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,					
RA	Ito J., Nishino H., Alimoto S., Kiyama H., Shiozaka S.;					
RT	"Expression and activity-dependent changes of a novel limbic-serine					
RT	protease gene in the hippocampus.";					
RL	J. Neurosci. 15:5088-5097(1995).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RA	Yoshida S., Hirata A., Inoue N., Shiozaka S.;					
RT	"Cloning and assignment of mouse neutropin gene, Prs619 to chromosome					
RT	7B4.";					
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBD databases.					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Czech II; TISSUE=Mammary gland;					

RX MEDLINE=22388257; PubMed=12477933; DOI=10.1073/pnas.242603899;
 RA Strausberg R. L., Feingold E. A., Grouse L. H., Derge J. G.,
 RA Klausner R. D., Collins F. S., Wagner L., Shenmen C. M., Schuler G. D.,
 RA Altshul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bat N. K.,
 RA Hopkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L.,
 RA Stapleton M., Soares M. B., Bonaldo M. F., Casavant T. L., Schetz T. E.,
 RA Brownstein W. J., Usdin T. B., Toshiyuki S., Carninci P., Prange C. C.,
 RA Raha S. S., Lottellano N. A., Peters G. J., Abramson R. D., Mullany S. J.,
 RA Bosak S. A., McEwan P. J., McKernan K. J., Malek J. A., Gunaratne P. H.,
 RA Richards S., Worley K. C., Hale S. S., Garcia A. M., Gay L. J., Hulik S. W.,
 RA Villalon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,
 RA Blakesley R. W., Touchman J. W., Green E. D., Dickson M. C.,
 RA Rodriguez A. C., Grimwood J., Schmutz J., Myers R. M.,
 RA Buterfield Y. S. N., Krzywinski M. I., Skalska U., Smallie D. E.,
 RA Scherch A., Schein J. E., Jones S. J. M., Marra M. A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RM [4]
 RP SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RC STRAIN-BALB/C; TISSUE=Brain;
 RX MEDLINE=96225202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
 RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
 RA Shiozaki T., Midorikawa R., Kamachi T., Kawabe A., Shiozaki S.;
 RT "Characterization of recombinant and brain neuropeptide, a plasticity-
 related serine protease.";
 RL J. Biol. Chem. 273:11189-11196(1998).
 RM [5]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
 RC TISSUE=Hippocampus;
 RX MEDLINE=99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
 RA Kishii T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
 RA Shiozaki S., Hakoshima T.;
 RT "Crystal structure of neuropeptide, a hippocampal protease involved in
 kindling epileptogenesis.";
 RL J. Biol. Chem. 274:4220-4224(1999).
 CC -1- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 hippocampal plasticity. Has a strong proteolytic activity against
 fibronectin.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-
 fluorophosphate, leupeptin and (4-aminodiphenyl)methanesulfonyl 1-
 fluoride.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed specifically in the limbic system of
 mouse brain and is localized at highest concentration in pyramidal
 neurons of the hippocampal CA1-3 subfields.
 CC -1- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260;
 CC NOTE=Ref. 4.
 CC -1- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
 CC NOTE=Ref. 4.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 subfamily.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; D30785; BA06451.1; -;
 DR EMBL; AB032202; AA82435.1; -;
 DR EMBL; BC055895; AA55895.1; -;
 DR PIR; I56559; I56559.
 DR PDB; INPM; X-ray; A/B=33-256.
 DR MEROPS; S01.244; -;
 DR MGd; MG1:892018; K1K8.
 DR InterPro; IPR009003; Pept_Ser_Cys.

DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
 KW Serine protease; Signal; Zymogen.
 FT SIGNAL 1 28
 FT PROPEP 29 32 Potential.
 FT CHAIN 33 260
 FT ACT_SITE 73 73 Neuropsin.
 FT ACT_SITE 120 120 Charge relay system (By similarity).
 FT ACT_SITE 212 212 Charge relay system (By similarity).
 FT DISULFID 39 173 Charge relay system (By similarity).
 FT DISULFID 58 74
 FT DISULFID 145 246
 FT DISULFID 152 218
 FT DISULFID 184 198
 FT DISULFID 208 233
 FT DISULFID 233 233
 FT CARBOHYD 110 110
 FT STRAND 34 34
 FT STRAND 37 38
 FT TURN 41 42
 FT TURN 41 42
 FT TURN 45 46
 FT STRAND 47 52
 FT TURN 53 54
 FT STRAND 55 64
 FT TURN 65 66
 FT STRAND 67 70
 FT HELIX 72 74
 FT STRAND 80 83
 FT STRAND 87 87
 FT TURN 88 89
 FT STRAND 96 98
 FT STRAND 100 105
 FT TURN 107 108
 FT TURN 114 115
 FT TURN 118 119
 FT STRAND 122 126
 FT STRAND 140 141
 FT TURN 148 149
 FT STRAND 151 156
 FT STRAND 170 178
 FT STRAND 172 178
 FT HELIX 181 187
 FT TURN 189 191
 FT TURN 194 195
 FT STRAND 196 200
 FT TURN 202 203
 FT STRAND 206 206
 FT TURN 209 210
 FT TURN 212 213
 FT STRAND 215 218
 FT TURN 219 220
 FT STRAND 221 228
 FT STRAND 235 235
 FT TURN 236 237
 FT STRAND 238 238
 FT STRAND 240 244
 FT HELIX 245 256
 SQ SEQUENCE 260 AA; 28523 MW; BE5FE6BE37CDD60E CRC64;

Query Match 45.3%; Score 622.5; DB 1; Length 260;
 Best Local Similarity 49.0%; Pred. No. 5.6e-42;
 Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

5 IFLLLCV---LGSQATPKPIFNGTEGGRNSOPWQVGLFEGTSLRGGCVLIIDHRWLTAA 61
 13 ILILLFEGAMAGLIRAGSKILGRCICPHSOPWQALFQGERLIGCVLVGDRWLTAA 72
 62 HCSGRYWLVLGHSLSQLDWTQIRHSGFSVTHPGYLGAS-TSHEHDLRLRLRPVAV 120

DB 73 HCKKQKYSVRLGHSLSQSRDQPEQIQAQSIQHPCCNNNSPDDHSDIWLIRLQANSYL 132
 QY 121 TSSVQPLPLPNDCAATAGTECHVGSGWGITNRPNPFPLDLCNLMSIVSHATCGVYPGRI 180
 DB 133 GDKVKFVQJLANLCPKVGQKIIISGMGVNPSQANFNTLCAVKKIYSQKCEKRAYPGKI 192
 QY 181 TSNMVCAGSVPGDACCQSGSGPLVCGGVYQGLVSGVSGVPCGQDGI PGVYTYICRYVDM 240
 DB 193 TEGMVCAGSSNGADTCQSGSGGPLVCDGMLQGITWSGS-DPCGKPKPGVYTKICRYTTW 251
 QY 241 IRMTMRN 247
 DB 252 IKKTMDN 258

RESULT 6
 ID_NRPN RAT STANDARD; PRT; 260 AA.
 AC 088780;
 DT 15-JUN-1999 (Rel. 38, Created)
 DT 15-JUN-1999 (Rel. 38, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
 protease 1).
 GN Name=KlK8; Synonyms=Bepl, N-tpn, Pres19;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer; TISSUE=Brain;
 RX MEDLINE=98389725; PubMed=9722524; DOI=10.1074/jbc.273.36.23004;
 RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
 RT "Serine proteases in rodent hippocampus."
 RL J. Biol. Chem. 273:23004-23011(1998).
 CC - FUNCTION: Suggested to be involved in kindling epileptogenesis and
 hippocampal plasticity. Has a strong proteolytic activity against
 fibronectin (By similarity).
 CC - CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC - SUBCELLULAR LOCATION: Secreted (By similarity).
 CC - TISSUE SPECIFICITY: Restricted to hippocampus.
 CC - SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 subfamily.

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 or send an email to license@ebi.ac.uk).

 CC EMBL; AJ005641; CA06643.1; -.
 DR HSSP; O61955; INPM.
 DR MEROPS; S01.244; -.
 DR InterPro; IPR009003; Pept Ser Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Hydrolase; Serine protease; Signal; Zymogen.
 FT SIGNAL 1 28 Potential.
 FT PROPEP 29 32 By similarity.
 FT CHAIN 33 260 Neuropsin.
 FT ACT_SITE 73 73 Charge relay system (By similarity).
 FT ACT_SITE 120 120 Charge relay system (By similarity).
 FT ACT_SITE 212 212 Charge relay system (By similarity).

PT DISULFID 39 173 By similarity.
PT DISULFID 58 74 By similarity.
PT DISULFID 145 246 By similarity.
PT DISULFID 152 218 By similarity.
PT DISULFID 184 198 By similarity.
PT DISULFID 208 233 By similarity.
PT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 260 AA; 28510 MM; 58DPAF0602A0B765 CRC64;
Query Match 45.2%; Score 621.5; DB 1; Length 260;
Best Local Similarity 48.6%; Pred. No. 6.7e-42;
Matches 118; Conservative 32; Mismatches 90; Indels 3; Gaps 3;
QY 5 IFFLL-CVILLSQATKRIKNGTCGGRNSQWQGLFEGTSLRCCGYLIDHRWLTAAHC 63
D 15 LFLMGAMAGITRQKSGKILGEGCKPSPQWQFALFQGERLVCGGVLVGRWVLTAAHC 74
QY 64 SGRHWVRLGHSLSQDWTREQIRHSGFSVTHPGVLAGS-TSHHDLRLRLRPREVTS 122
D 75 KKQKYSRLGDHSLOKXDEPQELQVARSICHPCFNSNPEDSHDMLRLQNSANLGD 134
QY 123 SVQPLPLPNDCAVATGTECHVSGMGTTHPRNPDPDLQCLNLSTVSHATCHGVYPRITS 182
D 135 KVKPEILANLCPKVGQKCIISGMGTVTSPOENFNTLNCAEVKTIYQNKCEBAYPGKITE 194
QY 183 NMVACAGVPQDADCGSGGGLVCGGVLCGLVSGVSPGCGDIPGYTYTICKYVWIR 242
D 195 GWCAGSSNADTQGGSGGLVCGGVLCGLVSGVSPGCGDIPGYTYTICKYVWIR 253
QY 243 MIM 245
D 254 KTM 256
RESULT 7
KLKB HUMAN STANDARD; PRT; 250 AA.
AC QGUBX7; Q75837; Q9NS65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kallikrein 11 precursor (EC 3.4.21.-) (Hippocastin) (Trypsin-like
DE protease) (UN0649/PRO1279).
GN Name=KLK11; Synonym=PRSS20, TLSP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RC MEDLINE=98438738; PubMed=9765601; DOI=10.1016/S0167-4781(98)00116-X;
RA Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shioaka S.;
RT "cDNA cloning and expression of a novel serine protease, TLSP.";
RL Biochim. Biophys. Acta 1399:225-228(1998).
RN (2)
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Hippocampus, and Prostate;
RC MEDLINE=20339229; PubMed=10872828; DOI=10.1006/birc.2000.2761;
RA Mitsui S., Yamada T., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "A novel isoform of a kallikrein-like protease, TLSP/hippocastin,
RT (PRSS20), is expressed in the human brain and prostate.";
RL Biochem. Biophys. Res. Commun. 272:205-211(2000).
RN (3)
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=20130117; PubMed=10662548; DOI=10.1006/geno.1999.6072;
RA Yousef G.M., Scortias A., Diamandis E.P.;
RT "Genomic organization, mapping, tissue expression, and hormonal
RT regulation of trypsin-like serine protease (TLSP PRSS20), a new member
RT of the human kallikrein gene family.";
RL Genomics 63:88-96(2000).
RN (4)
RP SEQUENCE FROM N.A. (ISOFORM 1).

RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN (5)
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Daniel B., Dowd P.,
RA Eason D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Shadigiri S., Simmons L., Singh U., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanebe C., Wleand D., Woods K., Xie M.-H., Yansuta D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.T.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN (6)
RP SEQUENCE FROM N.A.
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerzin J.E., Hellsten U., Goodstein D., Courtney O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth J., Bajorek E., Black S., Branscomb E.,
RA Canepaegel S., Carrano A.V., Caolile C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalin E., Delai P., Denys M., Deter J.C.,
RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hamon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Ierant S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Lartionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA Malfaciti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Ratterer J.,
RA Rodriguez A., Rogers S., Salamon A., Salazar A., She X., Smith D.,
RA Slezak T., Solovjev V., Thayer N., Tice H., Tsai M., Uexasawa A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.B.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19.";
RL Nature 428:529-535(2004).
RN (7)
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tomihyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skaleka U., Smalins D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Possible multifunctional protease. Efficiently cleaves
CC bz-phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and
CC weakly cleaves other substrates for kallikrein and trypsin.
CC -1- SUBCELLULAR LOCATION: Secreted.

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CC -!- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=G9UNX7-1; Sequence=displayed;
CC Name=2;
CC IsoId=G9UNX7-2; Sequence=VSP_005402;
CC -!- TISSUE SPECIFICITY: Expressed in brain; isoform 2 in prostate.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
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DR EMBL; AB012917; BAA3404.1; ALT_INIT.

DR EMBL; AB013730; BAA88713.1; -.

DR EMBL; AB041036; BAA96797.1; -.

DR EMBL; AF164623; AAD47815.1; -.

DR EMBL; AF243527; AAG33364.1; -.

DR EMBL; AY359014; AAO89373.1; -.

DR EMBL; AC011473; AAG23257.1; -.

DR EMBL; BC022068; AAG22068.1; -.

DR HSSP; P00760; 1EZK.

DR MEROPS; S01.257; -.

DR Genew; HGNC:6359; KTKL1.

DR H-INVD; HIX0015375; -.

DR MIM; 604434; -.

DR GO; GO:0008236; F:serine-type peptidase activity; TAS.

DR InterPro; IPR009003; Pept_Ser_Cys.

DR InterPro; IPR001254; Peptidase_S1.

DR Pfam; PF00089; Trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PROSITE; PSS0240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR KMW; KMW:Signal; Glycoprotein; Hydrolase; Serine protease;

FT SIGNAL; 1 18 Potential.

FT PROPEP; 19 21 Activation peptide (potential).

FT CHAIN; 22 250 Kallikrein 11.

FT ACT_SITE; 62 62 Charge relay system (By similarity).

FT ACT_SITE; 110 110 Charge relay system (By similarity).

FT ACT_SITE; 203 203 Charge relay system (By similarity).

FT DISULFID; 28 163 By similarity.

FT DISULFID; 47 63 By similarity.

FT DISULFID; 135 237 By similarity.

FT DISULFID; 142 209 By similarity.

FT DISULFID; 174 188 By similarity.

FT DISULFID; 199 224 By similarity.

FT CARBOHYD; 99 99 N-linked (GlcNAc...) (Potential).

FT CARBOHYD; 165 165 N-linked (GlcNAc...) (Potential).

FT CARBOHYD; 181 181 N-linked (GlcNAc...) (Potential).

FT CARBOHYD; 210 210 N-linked (GlcNAc...) (Potential).

FT VARSPLIC; 1 1 M -> MORLRMLRDMKSSGRLTAARSPARSSPLQAM (in isoform 2).

FT FTId=VSP_005402.

FT SQ SEQUENCE 250 AA; 27466 MW; 192D910BBCDC7A56 CRC64;

Query Match 45.0%; Score 618.5; DB 1; Length 250;

Best Local Similarity 48.2%; Pred. No. 1.1e-41;

Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;

QY 3 LSTFLLCVGLGSOATPKIFNGECGRNSOPMOVGLFEETSLRCGGVLIIDHRWVLTAAH 62

DB 4 LQILALALAGIVGGER-RIIKGFECPHSPQWAALEFETRLLCATLLAPRWLTAAH 62

QY 63 CSGRYVRLGHSLSQLDWTEQIRHSGSVTHPGYIGA--STSHHDLRLRLPLRVV 120

DB 63 CLKRYTHLGOHNLQKBECEQTRTATESFPHGFNNSLPNKHDRDMLVWMAKSPVSI 122

QY 121 TSSVQPLPLPNDCAITAGTECHSVSGMGITNHPRNPFDLLQCLNLSTYSHATCGVYGR 180

DB 123 TWAVRPLTSLRCCTAGTACTSLISGMSGTSSPOLRLPTTLKCANITLIEHOKCENAPGNT 182

QY 181 TSNMVCAG-GVPGQDACQSDSGGELVCGVLOGILVSWGSGVPGGQDIPGVYTYCKYVD 239

DB 183 TDTMVCASVQEGKDSQSDSGGELVCGVLOGILVSWG-DPCALTRKPGVYTYCKYVD 241

QY 240 WIRMIMRN 248

DB 242 WIGETMKN 250

RESULT 8

Q7JIG6 PRELIMINARY; PRT; 255 AA.

ID Q7JIG6 PRELIMINARY; PRT; 255 AA.

AC Q7JIG6;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE KX15.

OS *Saguinus oedipus* (Cotton-top tamarin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.

OX NCBI_TaxID=9490;

RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=21094033; PubMed=11177570; DOI=10.1089/104454900750058080;

RA Olsson A.Y., Persson A.M., Valtonen-Andre C., Lundvall A.;

RT "Glutathione S-transferase of the cotton-top tamarin: molecular cloning of the gene encoding the tissue kallikrein";

RU DNA Cell Biol. 19:721-727 (2000).

RN [2]

SEQUENCE FROM N.A.

RA Olsson Y., Persson M., Lundvall A.;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBS databases.

CC -!- SIMILARITY: Belongs to peptidase family S1.

DR EMBL; AF173845; BAA5302.1; -.

DR HSSP; P00761; 1AKS.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR009003; Pept_Ser_Cys.

DR Pfam; PF00089; Trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PSS0240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKOWN_1.

KW Hydrolase; Protease; Serine protease.

SQ SEQUENCE 255 AA; 28078 MW; A040914ABC8FECBD CRC64;

Query Match 44.5%; Score 611; DB 2; Length 255;

Best Local Similarity 49.4%; Pred. No. 4.6e-41;

Matches 118; Conservative 31; Mismatches 76; Indels 14; Gaps 5;

QY 21 KIFNGTECGRNSOPMOVGLFEETSLRCGGVLIIDHRWVLTAAHSGSRVWRLGHSLSQ 80

DB 20 KLEGEBCAPSPQWQVALYERGFNCAGSLSPHWLSSAAHQSRMRVRLGHNHUKR 79

QY 81 DMTQIRHSGSVTHPGYLAGSTHEHDLLRLPLRVYTSVQPLPLPNDCAITAGTEC 140

DB 80 DGPQLRTASRVLDHPYV--EARSHRDMLRLVGPAPRLTPVRLPVYLPTRCPHGEAC 137

QY 141 HVSGMGITNN-----PRN--FPDILQCLNLSTYSHATCGVYPGRTSNMVCAGV 190

DB 138 VVSGMGLVSNHNPETTORPOSQVSLPDTLHCANISITSDASCUKNYFGRLTNMVCAGAB 197

RT "Molecular cloning of the human kallikrein 15 gene (KLK15). Up-
RT regulation in prostate cancer." ;
RL J. Biol. Chem. 276:53-61 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed1054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McNally J.,
RA Moss P., Paepker B., Wang K. ;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region." ;
RL Gene 257:119-130 (2000).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94289486; PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;
RA Dhanich M.E., Spiess M. ;
RT "A novel serine proteinase-like sequence from human brain." ;
RL Biochim. Biophys. Acta 1218:225-228 (1994).
RN [4]
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E. ;
RT "An unappreciated role for RNA surveillance." ;
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC -1- FUNCTION: Protease whose physiological substrate is not yet known.
CC -1- SUBCELLULAR LOCATION: Secreted (probable).
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Name=1;
CC IsoId=Q9H2R5-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H2R5-2; Sequence=VSP_005405;
CC Note=May be produced at very_low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC Name=3;
CC IsoId=Q9H2R5-3; Sequence=VSP_005406, VSP_005407;
CC Name=4;
CC IsoId=Q9H2R5-4; Sequence=VSP_005404;
CC -1- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
CC expressed in the prostate, salivary, and adrenal glands and in the
CC colon testis and kidney.
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AF242195; AACG94949.1; -
DR EMBL; AF242195; AACG9470.1; -
DR EMBL; AF242195; AACG9471.1; -
DR EMBL; AF242195; AACG9472.1; -
DR EMBL; AF243527; AACG33354.1; -
DR EMBL; X75363; CAAS3145.1; ALT_SEQ.
DR HSSP; P00760; 1EXX.
DR MEROPS; S01.081; -
DR Genew; HGNC:20453; KLK15.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0004252; C:serine-type endopeptidase activity; NAS.
DR GO; GO:0006508; F:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Pept_ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRY_SP_1.
DR PROSITE; PS00240; TRYPSIN_DOM_1.
DR PROSITE; PS00134; TRYPSIN_HIS_1.
DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.

KM Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
KW Signal; Zymogen.
FT SIGNAL 1 16 Potential.
FT PROPEP 17 21 Activation peptide (potential).
FT CHAIN 22 256 Kallikrein 15.
FT ACT_SITE 62 62 Charge relay system (By similarity).
FT ACT_SITE 106 106 Charge relay system (By similarity).
FT ACT_SITE 209 209 Charge relay system (By similarity).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (potential).
FT CARBOHYD 232 232 N-linked (GlcNAc...) (potential).
FT VARSPLIC 122 206 Missing (in isoform 4).
FT VARSPLIC 122 256 Missing (in isoform 2).
FT VARSPLIC 161 161 Missing (in isoform 3).
FT VARSPLIC 161 161 /FtId=VSP_005405.
FT VARSPLIC 162 256 /FtId=VSP_005406.
FT VARSPLIC 162 256 Missing (in isoform 3).
FT CONFLICT 147 160 SHNEBGTGSPRSQ -> PLSSP (in Ref. 2).
FT SEQUENCE 256 AA; 28087 MW; B5EBF6D6022786B5 CRC64;
SQ
Query Match 43.6%; Score 599; DB 1; Length 256;
Best Local Similarity 47.1%; Pred. No. 4.2e-40;
Matches 121; Conservative 32; Mismatches 88; Indels 16; Gaps 6;
QY 5 IFLLCVLSQANT--PKIFNGTCGRNSQPMQVGLPEGTSLRGCVLIDHRWVLTAAH 62
Db 3 LLTLTFLTAATAADGDKLGEBCAPSPQWQALTRERFNGASLSPHWLSAAH 62
QY 63 CGSGRYWVRLGSHLSQLDWTEQIRHSGFVYTHRGYLCASTSHHDLRLRLRPVRYTS 122
Db 63 CQSPFMRRLGHEHNLKRKDGPEQLRTTSRVLPHRRY--EASSHNDILTLVGPARNLP 120
QY 123 SVQPLPLPNDCAATGTCGHSWGKGTNH-----PNN--PFPDLGLCLSLYSNATC 172
Db 121 QVRPAVLPTRCPHGEACVVSQWGLVSHNEBGTAGSPRSQVSLPDTLHCANVISIISDSC 180
QY 173 HGVPGRGRTSMWVAGV--PGQDAACGGSGGPLVCGVGLGVLGVSVCPCGDSIPGVY 231
Db 181 DKSLPGRLLTMVCCAGAEGRGASCBDSGSLVCGGLVSGNDV--PCDNTTKPQVY 239
QY 232 TYICKYVDMIMRN 248
Db 240 TKVCHYLEWIRETMKRN 256
RESULT 14
QOQYN4 PRELIMINARY; PRT; 249 AA.
ID QOQYN4
AC QOQYN4
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE HippoStasin.
GN Name=2310015108Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
RA Mitsui S., Okui A., Komitani K., Uemura H., Yamaguchi N. ;
RT "cDNA cloning and tissue-specific splicing variants of mouse
RT hippoStasin/TUSP (PRSS20)." ;
RL Biochim. Biophys. Acta 1494:206-210 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Yamaguchi N., Mitsui S. ;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;

Query March 43.5%; Score 597.5; DB 2; Length 276;
Best Local Similarity 47.0%; Pred. No. 6e-40;
Matches 118; Conservative 33; Mismatches 95; Indels 5; Gaps 4;

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QY 1 MGLSIFLLCVLGLSQATPKIFENGTEGGRNSQPMQVGLFEGTSLRCGVLIDHRWVLA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 28 MTLRLIALALVTGHVGET-RIIKGYECRPHSQPMQVALFQKTRLGATLIAPKMLLTA 86
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AHCGSGRYWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEDRLRLRLPV 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 AHCRKPHYVILGHEHNEKTDGCEORRMATESFPHDPFNNSLPNKHDRNDIMLVKMSSPV 146
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 119 RVTSSVQPLPLPNDCAATAGTECHVSGMGITNHPNPPDLLOCLNLSIVSHATCHGVYPG 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 147 PFTPAVQPLTISPFCVANGTSCGISGWTSSFQRLRPHSLRCANVSIIEHKECEKAYPG 206
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 179 RITSNMVCAQ-GVPGDACAQDSSGAPLVCGGVLOGLVSWGSGVPGQGDGIPGVYTYICKY 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 207 NITDTMLCASVRKKGKDSQCGDSGSPLYCNGSLQGIISWGQ-DPCAVTRKPGVYTTKVCXY 265
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 238 VDWIRMIMRNN 248
   :|||:|||||
Db 266 FNMWIEYVMRNN 276
   :|||:|||||
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Search completed: March 5, 2005, 18:20:29
Job time : 178 secs

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OM protein - protein search, using sw model

Run on: March 5, 2005, 18:02:28 ; Search time 43 Seconds
(without alignment)
430.534 Million cell updates/sec

Title: US-10-006-116A-194
Perfect score: 1374
Sequence: 1 MGSLIFLLCVGLHSQATP.....GVYTYCKYDWMIRNN 248

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1359.5	98.9	249	4	US-09-949-016-8151
2	1301	94.7	254	4	US-09-949-016-6948
3	811	59.0	162	4	US-09-244-111-6
4	630.5	45.9	260	4	US-09-618-259-7
5	626.5	45.6	260	3	US-09-070-526-2
6	622.5	45.3	260	3	US-09-025-059-3
7	622.5	45.3	260	4	US-09-008-271A-7
8	622.5	45.3	260	4	US-09-618-259-8
9	618.5	45.0	250	4	US-09-205-258-427
10	618.5	45.0	282	3	US-09-025-059-1
11	602.5	43.9	288	4	US-09-386-642-13
12	598.5	43.6	289	4	US-09-386-642-14
13	597.5	43.5	248	3	US-08-944-483-24
14	573	41.7	247	2	US-08-956-267A-2
15	567	41.3	290	4	US-09-949-016-8166
16	564.5	41.1	270	4	US-09-949-016-7712
17	564.5	41.1	293	4	US-09-503-908-2
18	564	41.0	276	1	US-08-467-155A-1
19	564	41.0	276	2	US-08-628-198-1
20	564	41.0	276	3	US-09-201-038-1
21	564	41.0	276	5	PCT-US96-07343-1
22	563	41.0	325	4	US-09-949-016-7713
23	561	40.8	244	1	US-08-361-395-1
24	555	40.4	253	2	US-08-557-146-2
25	555	40.4	253	2	US-08-824-874-3
26	555	40.4	253	2	US-09-154-344-2
27	555	40.4	253	3	US-08-930-188-2

28	555	40.4	253	3	US-09-210-084-3	Sequence 3, Appli
29	555	40.4	253	4	US-09-764-762-3	Sequence 3, Appli
30	555	40.4	253	5	PCT-US96-04294-2	Sequence 2, Appli
31	555	40.4	265	4	US-09-949-016-7716	Sequence 7716, Ap
32	552	40.2	229	1	US-09-120-582-2	Sequence 2, Appli
33	547	39.8	223	1	US-08-278-091-9	Sequence 9, Appli
34	547	39.8	223	1	US-08-483-859-9	Sequence 9, Appli
35	547	39.8	223	1	US-08-472-173-9	Sequence 9, Appli
36	547	39.8	223	2	US-08-487-167-9	Sequence 9, Appli
37	547	39.8	223	2	US-08-487-816-9	Sequence 9, Appli
38	547	39.8	223	2	US-08-286-149-9	Sequence 9, Appli
39	547	39.8	223	3	US-08-801-499-9	Sequence 9, Appli
40	547	39.8	223	2	US-08-615-271-9	Sequence 9, Appli
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42	547	39.8	223	3	US-09-074-659-9	Sequence 9, Appli
43	547	39.8	223	3	US-09-106-468-9	Sequence 9, Appli
44	547	39.8	223	3	US-09-106-466A-9	Sequence 9, Appli
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46	547	39.8	223	4	US-09-601-318-2	Sequence 2, Appli
47	546	39.7	244	4	US-09-618-259-11	Sequence 11, Appli
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52	544.5	39.6	291	2	US-08-628-198-11	Sequence 11, Appli
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56	540	39.3	224	3	US-08-944-403-33	Sequence 33, Appli
57	529.5	38.5	225	2	US-08-557-146-12	Sequence 12, Appli
58	529.5	38.5	225	2	US-09-154-344-12	Sequence 12, Appli
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78	503	36.6	263	3	US-08-807-151-5	Sequence 5, Appli
79	503	36.6	263	3	US-09-210-084-5	Sequence 5, Appli
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82	501	36.5	254	4	US-09-949-016-8770	Sequence 8770, Ap
83	498	36.2	254	3	US-09-439-313-525	Sequence 525, App
84	498	36.2	254	4	US-09-636-215-525	Sequence 525, App
85	498	36.2	254	4	US-09-685-166A-525	Sequence 525, App
86	498	36.2	254	4	US-09-679-466-525	Sequence 525, App
87	498	36.2	254	4	US-09-759-143-525	Sequence 525, App
88	498	36.2	254	4	US-09-651-236-525	Sequence 525, App
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93	497	36.2	258	1	US-08-744-026-3	Sequence 3, Appli
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95	497	36.2	258	3	US-09-261-767-3	Sequence 3, Appli
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98	496.5	36.1	248	3	US-09-261-767-1	Sequence 1, Appli
99	494	36.0	254	3	US-09-439-313-523	Sequence 523, App
100	494	36.0	254	4	US-09-636-215-523	Sequence 523, App

101	494	36.0	254	4	US-09-685-166A-523	Sequence 523, App	174	458	33.3	228	2	US-08-296-149-7	Sequence 7, Appli
102	494	36.0	254	4	US-09-679-426-523	Sequence 523, App	175	458	33.3	228	2	US-08-801-499-7	Sequence 7, Appli
103	494	36.0	254	4	US-09-759-143-523	Sequence 523, App	176	458	33.3	228	2	US-08-615-271-7	Sequence 7, Appli
104	494	36.0	254	4	US-09-651-236-523	Sequence 523, App	177	458	33.3	228	3	US-09-074-660-7	Sequence 7, Appli
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108	493	35.9	262	2	US-08-824-874-4	Sequence 4, Appli	181	458	33.3	228	3	US-09-106-466A-7	Sequence 7, Appli
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110	493	35.9	262	3	US-09-210-084-4	Sequence 4, Appli	183	457.5	33.3	237	3	US-08-767-820A-1	Sequence 7, Appli
111	493	35.9	262	3	US-09-478-957-4	Sequence 4, Appli	184	457.5	33.3	237	3	US-08-622-046B-7	Sequence 7, Appli
112	493	35.8	225	2	US-09-764-762-4	Sequence 4, Appli	185	457.5	33.3	237	3	US-08-944-483-38	Sequence 7, Appli
113	492	35.8	225	2	US-09-027-337-5	Sequence 5, Appli	186	457.5	33.3	237	3	US-09-100-264-3	Sequence 3, Appli
114	492	35.8	225	4	US-09-644-600-5	Sequence 5, Appli	187	457.5	33.3	237	4	US-09-303-339-2	Sequence 2, Appli
115	492	35.8	225	4	US-09-654-600A-5	Sequence 5, Appli	188	457.5	33.3	237	4	US-08-843-076D-7	Sequence 7, Appli
116	492	35.8	262	1	US-08-744-026-4	Sequence 4, Appli	189	457.5	33.2	237	4	US-09-103-008-1	Sequence 7, Appli
117	492	35.8	262	2	US-09-102-732-4	Sequence 4, Appli	190	455.5	33.2	237	1	US-08-096-946-11	Sequence 1, Appli
118	492	35.8	222	3	US-09-261-767-4	Sequence 3, Appli	191	455.5	33.2	237	5	PCT-US94-07329-11	Sequence 11, Appli
119	491	35.7	221	4	US-09-959-392-33	Sequence 33, Appli	192	455.5	33.2	237	5	PCT-US95-06157-1	Sequence 11, Appli
120	490	35.7	224	3	US-08-944-483-34	Sequence 34, Appli	193	455.5	33.2	261	3	US-08-768-859A-19	Sequence 19, Appli
121	487.5	35.5	449	4	US-09-636-215-617	Sequence 617, App	194	455.5	33.2	261	3	US-08-767-820A-19	Sequence 19, Appli
122	487.5	35.5	449	4	US-09-685-166A-617	Sequence 617, App	195	455.5	33.2	261	3	US-08-622-046B-3	Sequence 3, Appli
123	487.5	35.5	449	4	US-09-679-426-617	Sequence 617, App	196	454.5	33.1	232	2	US-08-897-340-31	Sequence 31, Appli
124	487.5	35.5	449	4	US-09-759-143-617	Sequence 617, App	197	454.5	33.1	232	3	US-09-252-329-31	Sequence 31, Appli
125	487.5	35.5	449	4	US-09-651-236-617	Sequence 617, App	198	454.5	33.1	244	5	PCT-US95-06157-10	Sequence 31, Appli
126	487	35.4	449	4	US-09-651-236-617	Sequence 617, App	199	454.5	32.9	248	5	US-09-651-236-617-8	Sequence 8, Appli
127	487	35.4	224	2	US-08-766-982-13	Sequence 617, App	200	452.5	32.9	244	3	US-08-768-859A-10	Sequence 10, Appli
128	487	35.4	224	3	US-08-944-483-36	Sequence 36, Appli	201	452.5	32.9	244	3	US-08-767-820A-10	Sequence 10, Appli
129	478	34.8	224	3	US-09-296-219-13	Sequence 13, Appli	202	452.5	32.9	244	3	US-08-622-046B-16	Sequence 16, Appli
130	472.5	34.4	220	3	US-09-439-313-327	Sequence 35, Appli	203	452.5	32.9	244	4	US-08-843-076D-5	Sequence 5, Appli
131	472.5	34.4	220	3	US-09-352-616A-327	Sequence 327, App	204	452.5	32.9	237	2	US-08-818-547-2	Sequence 5, Appli
132	472.5	34.4	220	4	US-09-232-149A-327	Sequence 327, App	205	450.5	32.8	237	3	US-08-768-859A-16	Sequence 2, Appli
133	472.5	34.4	220	4	US-09-636-215-327	Sequence 327, App	206	450.5	32.8	237	3	US-08-767-820A-16	Sequence 16, Appli
134	472.5	34.4	220	4	US-09-685-166A-327	Sequence 327, App	207	450.5	32.8	237	3	US-08-622-046B-12	Sequence 12, Appli
135	472.5	34.4	220	4	US-09-679-426-337	Sequence 327, App	208	450.5	32.8	237	3	US-08-944-483-37	Sequence 37, Appli
136	472.5	34.4	220	4	US-09-759-143-327	Sequence 327, App	209	450.5	32.8	237	3	US-09-100-264-1	Sequence 1, Appli
137	472.5	34.4	220	4	US-09-651-236-327	Sequence 327, App	210	450.5	32.8	237	3	US-08-843-076D-1	Sequence 1, Appli
138	472.5	34.4	220	4	US-09-618-259-9	Sequence 9, Appli	211	450.5	32.8	237	4	US-08-943-076D-1	Sequence 1, Appli
139	472.5	34.4	262	4	US-08-744-026-5	Sequence 5, Appli	212	450.5	32.8	238	3	US-08-768-859A-8	Sequence 8, Appli
140	470.5	34.2	261	2	US-09-103-732-5	Sequence 5, Appli	213	450.5	32.8	260	3	US-08-983-075D-9	Sequence 9, Appli
141	470.5	34.2	261	3	US-09-083-521-6	Sequence 6, Appli	214	450.5	32.8	238	3	US-08-767-820A-21	Sequence 21, Appli
142	470.5	34.2	261	3	US-09-261-767-5	Sequence 5, Appli	215	450	32.6	244	3	US-08-622-046B-10	Sequence 10, Appli
143	470.5	34.2	261	4	US-09-413-049-1	Sequence 1, Appli	216	449.5	32.6	237	4	US-08-096-946-10	Sequence 8, Appli
144	470.5	34.2	261	4	US-09-907-402-1	Sequence 1, Appli	217	448.5	32.6	237	5	PCT-US94-07329-16	Sequence 16, Appli
145	470.5	34.2	261	4	US-09-618-259-9	Sequence 10, Appli	218	448.5	32.6	237	5	US-08-768-859A-21	Sequence 21, Appli
146	470.5	34.2	261	4	US-09-944-483-39	Sequence 39, Appli	219	447.5	32.6	237	3	US-08-622-046B-1	Sequence 1, Appli
147	470.5	34.2	271	2	US-08-628-198-10	Sequence 10, Appli	220	447.5	32.6	237	3	US-09-100-264-12	Sequence 12, Appli
148	470	34.2	271	2	US-08-628-198-10	Sequence 10, Appli	221	447.5	32.6	237	4	US-08-843-076D-8	Sequence 8, Appli
149	469.5	34.2	271	2	US-08-628-198-10	Sequence 10, Appli	222	447.5	32.6	237	4	US-09-146-831-1	Sequence 1, Appli
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151	469.5	34.2	271	2	US-08-628-198-10	Sequence 10, Appli	224	447.5	32.6	237	4	US-09-146-831-1	Sequence 1, Appli
152	469.5	34.2	271	2	US-08-628-198-10	Sequence 10, Appli	225	445	32.4	240	1	US-09-146-831-1	Sequence 1, Appli
153	469.5	34.2	271	2	US-08-628-198-10	Sequence 10, Appli	226	445	32.4	240	1	US-09-146-831-1	Sequence 1, Appli
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155	464.5	33.8	286	2	US-08-628-198-9	Sequence 9, Appli	228	445	32.4	240	3	US-08-439-313-176	Sequence 176, App
156	464.5	33.8	286	5	US-09-201-038-9	Sequence 9, Appli	229	430	31.3	299	1	US-09-352-616A-176	Sequence 176, App
157	464.5	33.8	286	5	PCT-US96-07343-9	Sequence 9, Appli	230	430	31.3	299	2	US-09-232-149A-176	Sequence 176, App
158	460.5	33.5	261	5	PCT-US95-06157-6	Sequence 6, Appli	231	430	31.3	299	4	US-09-159-812-176	Sequence 176, App
159	459	33.4	262	3	US-09-664-595A-15	Sequence 15, Appli	232	426.5	31.0	205	3	US-09-636-115-176	Sequence 176, App
160	459	33.4	262	3	US-09-025-059-4	Sequence 4, Appli	233	426.5	31.0	205	4	US-09-685-166A-176	Sequence 176, App
161	459	33.4	262	4	US-09-755-100A-14	Sequence 14, Appli	234	426.5	31.0	205	4	US-09-115-453-176	Sequence 176, App
162	458.5	33.4	261	3	US-08-768-859A-6	Sequence 6, Appli	235	426.5	31.0	205	4	US-09-688-489-176	Sequence 176, App
163	458.5	33.4	261	3	US-08-767-820A-6	Sequence 6, Appli	236	426.5	31.0	205	4	US-09-679-426-176	Sequence 176, App
164	458.5	33.4	261	3	US-08-622-046B-14	Sequence 14, Appli	237	426.5	31.0	205	4	US-09-759-143-176	Sequence 176, App
165	458.5	33.4	261	3	US-09-100-264-7	Sequence 7, Appli	238	426.5	31.0	205	4	US-09-651-236-176	Sequence 176, App
166	458.5	33.4	261	3	US-08-983-075D-3	Sequence 3, Appli	239	426.5	31.0	205	4	US-09-244-111-4	Sequence 176, App
167	458.5	33.4	261	4	US-08-843-076D-3	Sequence 7, Appli	240	426.5	31.0	205	4	US-08-738-413B-9	Sequence 9, Appli
168	458.5	33.4	228	4	US-09-949-016-7711	Sequence 7711, Ap	241	426.5	31.0	205	4	US-08-738-413B-9	Sequence 9, Appli
169	458	33.3	228	1	US-08-278-091-7	Sequence 7, Appli	242	426.5	31.0	205	4	US-08-738-413B-9	Sequence 9, Appli
170	458	33.3	228	1	US-08-483-859-7	Sequence 7, Appli	243	426.5	31.0	205	4	US-08-738-413B-9	Sequence 9, Appli
171	458	33.3	228	1	US-08-472-173-7	Sequence 7, Appli	244	426.5	31.0	205	4	US-08-738-413B-9	Sequence 9, Appli
172	458	33.3	228	2	US-08-487-167-7	Sequence 7, Appli	245	418	30.4	207	4	US-08-738-413B-9	Sequence 9, Appli
173	458	33.3	228	2	US-08-482-816-7	Sequence 7, Appli	246	417.5	30.4	233	2	US-08-738-413B-9	Sequence 9, Appli

247	406.5	29.6	231	4	US-09-402-515A-16	Sequence 16, Appl	320	354	25.8	461	6	5270178-18	Patent No. 5270178
248	404	29.4	234	1	US-08-684-862-6	Sequence 6, Appl	321	354	25.8	461	6	5270178-17	Patent No. 5270178
249	393	28.6	235	1	US-08-684-862-5	Sequence 5, Appl	322	354	25.8	461	6	5270178-18	Patent No. 5270178
250	389	28.3	236	2	US-08-738-413B-10	Sequence 10, Appl	323	353.5	25.7	230	3	US-08-944-483-62	Sequence 62, Appl
251	387	28.2	253	6	5223425-8	Patent No. 5223425	324	353.5	25.7	270	2	US-08-978-404B-8	Sequence 8, Appl
252	387	28.2	253	6	5223425-8	Patent No. 5223425	325	353.5	25.7	274	2	US-08-978-404B-8	Sequence 5, Appl
253	385.5	28.1	267	4	US-09-949-016-9575	Sequence 9575, Ap	326	353	25.7	314	3	US-09-008-217A-3	Sequence 6, Appl
254	385	28.0	232	2	US-08-738-413B-11	Patent No. 5223425	327	353	25.7	314	4	US-09-023-942A-6	Sequence 257, App
255	385	28.0	250	6	5223425-4	Patent No. 5223425	328	353	25.7	314	4	US-09-907-754A-257	Sequence 257, App
256	385	28.0	250	6	5223425-4	Patent No. 5223425	329	353	25.7	314	4	US-09-905-125A-257	Sequence 257, App
257	377.5	27.5	154	3	US-09-261-416-5	Sequence 5, Appl	330	353	25.7	314	4	US-09-902-775A-257	Sequence 257, App
258	374.5	27.3	238	6	5223425-5	Patent No. 5223425	331	353	25.7	314	4	US-09-906-700-557	Sequence 257, App
259	374.5	27.3	238	6	5223425-5	Patent No. 5223425	332	353	25.7	314	4	US-09-903-603A-257	Sequence 257, App
260	374.5	27.3	259	6	5223425-2	Patent No. 5223425	333	353	25.7	314	4	US-09-904-920A-257	Sequence 257, App
261	374.5	27.3	259	6	5223425-2	Patent No. 5223425	334	353	25.7	314	4	US-09-909-064-257	Sequence 257, App
262	374	27.2	260	6	5223425-10	Patent No. 5223425	335	353	25.7	314	4	US-09-905-381A-257	Sequence 257, App
263	374	27.2	260	6	5223425-10	Patent No. 5223425	336	353	25.7	314	4	US-09-906-618-257	Sequence 257, App
264	370.5	27.0	228	3	US-08-944-483-44	Sequence 44, Appl	337	351.5	25.6	814	1	US-08-750-711-1	Sequence 1, Appl
265	370	26.9	418	4	US-09-370-838-62	Sequence 62, Appl	338	349.5	25.4	166	4	US-09-636-215-838	Sequence 838, App
266	370	26.9	418	4	US-09-854-133-62	Sequence 62, Appl	339	349.5	25.4	166	4	US-09-685-166A-838	Sequence 838, App
267	368	26.8	418	1	US-08-508-448C-25	Sequence 25, Appl	340	349.5	25.4	166	4	US-09-679-426-838	Sequence 838, App
268	368	26.8	418	4	US-09-370-838-62	Sequence 82, Appl	341	349.5	25.4	166	4	US-09-759-143-838	Sequence 838, App
269	368	26.8	418	4	US-09-370-838-83	Sequence 83, Appl	342	349.5	25.4	166	4	US-09-651-236-838	Sequence 838, App
270	368	26.8	418	4	US-09-854-133-82	Sequence 82, Appl	343	349	25.4	159	3	US-09-020-956-172	Sequence 172, App
271	368	26.8	418	4	US-09-854-133-83	Sequence 83, Appl	344	349	25.4	159	3	US-09-030-607-172	Sequence 172, App
272	366.5	26.7	149	3	US-09-518-046-20	Sequence 20, Appl	345	349	25.4	159	3	US-09-439-313-172	Sequence 172, App
273	366	26.6	232	1	US-08-508-448C-19	Sequence 19, Appl	346	349	25.4	159	3	US-09-352-616A-172	Sequence 172, App
274	366	26.6	234	2	US-08-738-413B-12	Sequence 12, Appl	347	349	25.4	159	4	US-09-232-149A-172	Sequence 172, App
275	365.5	26.6	245	3	US-08-906-769-121	Sequence 121, App	348	349	25.4	159	4	US-09-159-812-172	Sequence 172, App
276	365.5	26.6	245	3	US-08-906-616-121	Sequence 121, App	349	349	25.4	159	4	US-09-636-215-172	Sequence 172, App
277	365.5	26.6	245	3	US-08-639-075A-121	Sequence 121, App	350	349	25.4	159	4	US-09-685-166A-172	Sequence 172, App
278	365.5	26.6	245	3	US-09-012-431-121	Sequence 121, App	351	349	25.4	159	4	US-09-115-453-172	Sequence 172, App
279	365.5	26.6	245	3	US-09-012-692-121	Sequence 121, App	352	349	25.4	159	4	US-09-688-489-172	Sequence 172, App
280	365.5	26.6	245	3	US-09-906-613-121	Sequence 121, App	353	349	25.4	159	4	US-09-679-426-172	Sequence 172, App
281	364.5	26.5	400	3	US-09-004-731-30	Sequence 30, Appl	354	349	25.4	159	4	US-09-759-143-172	Sequence 172, App
282	364.5	26.5	400	3	US-09-004-731-33	Sequence 33, Appl	355	349	25.4	159	4	US-09-651-236-172	Sequence 172, App
283	364.5	26.5	400	3	US-08-749-699-30	Sequence 30, Appl	356	349	25.4	1019	1	US-08-296-014A-4	Sequence 4, Appl
284	364.5	26.5	400	3	US-08-749-699-33	Sequence 33, Appl	357	349	25.4	1019	2	US-08-596-405-4	Sequence 4, Appl
285	364.5	26.5	400	4	US-09-004-729-30	Sequence 30, Appl	358	349	25.4	1019	2	US-08-877-620-4	Sequence 4, Appl
286	364.5	26.5	400	4	US-09-004-729-33	Sequence 33, Appl	359	349	25.4	1019	4	US-09-287-368-4	Sequence 4, Appl
287	362.5	26.4	242	3	US-09-004-731-36	Sequence 36, Appl	360	349	25.4	1019	4	US-09-626-795-4	Sequence 4, Appl
288	362.5	26.4	242	3	US-08-749-699-36	Sequence 36, Appl	361	349	25.4	1083	1	US-08-296-014A-2	Sequence 2, Appl
289	362.5	26.4	242	4	US-09-004-729-36	Sequence 36, Appl	362	349	25.4	1083	2	US-08-596-405-2	Sequence 2, Appl
290	362.5	26.4	319	4	US-09-386-642-12	Sequence 12, Appl	363	349	25.4	1083	2	US-08-877-620-2	Sequence 2, Appl
291	362.5	26.4	328	4	US-09-386-642-11	Sequence 11, Appl	364	349	25.4	1083	4	US-09-287-368-2	Sequence 2, Appl
292	361.5	26.3	387	3	US-09-032-215-8	Sequence 8, Appl	365	349	25.4	1083	4	US-09-626-795-2	Sequence 2, Appl
293	361.5	26.3	387	3	US-09-032-215-13	Sequence 13, Appl	366	348	25.3	461	6	5460953-3	Patent No. 5460953
294	361	26.3	236	1	US-08-684-862-4	Sequence 4, Appl	367	348	25.3	461	6	5460953-3	Patent No. 5460953
295	360.5	26.2	299	3	US-08-944-483-66	Sequence 66, Appl	368	347	25.3	262	1	US-07-720-189-1	Sequence 1, Appl
296	358	26.1	232	4	US-09-959-392-31	Sequence 31, Appl	369	347	25.3	356	4	US-09-054-272-18	Sequence 18, Appl
297	358	26.1	812	4	US-08-991-761A-7	Sequence 7, Appl	370	347	25.3	356	4	US-09-054-272-18	Sequence 18, Appl
298	357.5	26.0	232	3	US-08-906-769-81	Sequence 81, Appl	371	347	25.3	409	3	US-09-055-872-2	Sequence 2, Appl
299	357.5	26.0	232	3	US-08-906-616-81	Sequence 81, Appl	372	347	25.3	409	3	US-09-667-570A-2	Sequence 2, Appl
300	357.5	26.0	232	3	US-08-817-795-81	Sequence 81, Appl	373	347	25.3	410	3	US-09-065-872-1	Sequence 1, Appl
301	357.5	26.0	232	3	US-08-639-075A-81	Sequence 81, Appl	374	347	25.3	419	1	US-09-667-570A-1	Sequence 1, Appl
302	357.5	26.0	232	3	US-09-012-431-81	Sequence 81, Appl	375	347	25.3	419	2	US-08-295-411-1	Sequence 1, Appl
303	357.5	26.0	232	3	US-09-012-692-81	Sequence 81, Appl	376	347	25.3	419	4	US-08-955-411-1	Sequence 1, Appl
304	357.5	26.0	232	3	US-08-906-613-81	Sequence 81, Appl	377	347	25.3	419	4	US-09-657-570A-3	Sequence 3, Appl
305	357.5	26.0	232	3	PCT-US95-14442A-81	Sequence 81, Appl	378	347	25.3	419	4	US-10-182-263-3	Sequence 3, Appl
306	357	26.0	268	4	US-09-949-016-10712	Sequence 10712, A	379	347	25.3	460	5	PCT-US92-10242-1	Sequence 1, Appl
307	356.5	25.9	248	3	US-08-944-483-63	Sequence 63, Appl	379	347	25.3	460	2	US-08-756-506-2	Sequence 2, Appl
308	355.5	25.9	148	4	US-09-618-259-2	Sequence 2, Appl	380	347	25.3	460	2	US-08-756-506-6	Sequence 4, Appl
309	355.5	25.9	231	2	US-09-027-337-6	Sequence 6, Appl	381	347	25.3	461	4	US-10-182-263-2	Sequence 2, Appl
310	355.5	25.9	231	4	US-09-644-600-6	Sequence 6, Appl	382	347	25.3	461	4	US-09-054-272-32	Sequence 32, Appl
311	355.5	25.9	231	4	US-09-654-600A-6	Sequence 6, Appl	383	347	25.3	461	4	US-09-949-016-5921	Sequence 5921, Ap
312	355.5	25.9	276	2	US-09-016-366A-15	Sequence 15, Appl	384	347	25.3	461	6	5225537-2	Patent No. 5225537
313	355.5	25.9	276	2	US-08-978-404B-21	Sequence 21, Appl	385	347	25.3	485	4	US-09-949-016-10882	Sequence 10882, A
314	354.5	25.8	461	6	5270178-2	Patent No. 5270178	386	347	25.2	791	1	US-08-643-219-1	Sequence 1, Appl
315	354.5	25.8	461	6	5270178-2	Patent No. 5270178	387	346.5	25.2	791	3	US-08-851-350-1	Sequence 1, Appl
316	354	25.8	229	2	US-08-557-146-13	Sequence 13, Appl	388	346	25.2	234	3	US-08-944-483-16	Sequence 16, Appl
317	354	25.8	229	2	US-09-154-344-13	Sequence 13, Appl	389	346	25.2	241	3	US-08-944-483-59	Sequence 59, Appl
318	354	25.8	312	4	US-09-023-942A-4	Sequence 4, Appl	391	346	25.2	419	4	US-10-182-263-5	Sequence 5, Appl
319	354	25.8	461	6	5270178-17	Patent No. 5270178	392	346	25.2	419	4	US-10-182-263-6	Sequence 6, Appl

393	345.5	25.1	248	3	US-08-906-769-111	Sequence 111, App	466	339.5	24.7	253	3	US-09-578-303-4	Sequence 4, Appl1
394	345.5	25.1	248	3	US-08-906-616-111	Sequence 111, App	467	339.5	24.7	258	1	US-07-990-301A-2	Sequence 2, Appl1
395	345.5	25.1	248	3	US-08-817-795-111	Sequence 111, App	468	339.5	24.7	333	4	US-08-991-761A-8	Sequence 8, Appl1
396	345.5	25.1	248	3	US-08-639-075A-111	Sequence 111, App	469	339.5	24.7	419	4	US-10-182-263-4	Sequence 4, Appl1
397	345.5	25.1	248	3	US-09-012-431-111	Sequence 111, App	470	339	24.7	461	3	US-08-742-877-2	Sequence 2, Appl1
398	345.5	25.1	248	3	US-09-012-692-111	Sequence 111, App	471	339	24.7	461	3	US-09-053-871A-21	Sequence 21, Appl1
399	345.5	25.1	248	3	US-08-906-613-111	Sequence 111, App	472	339	24.7	461	4	US-10-133-907-5	Sequence 5, Appl1
400	345.5	25.1	248	3	PCT-US95-14442A-111	Sequence 111, App	473	339	24.7	461	6	5521070-2	Patent No. 5521070
401	344	25.0	274	2	US-09-016-366A-21	Sequence 21, Appl	474	339	24.7	461	6	5521070-2	Patent No. 5521070
402	344	25.0	274	2	US-08-978-404B-16	Sequence 16, Appl	475	339	24.7	480	4	US-09-949-016-11123	Sequence 11123, A
403	343.5	25.0	273	2	US-08-978-404B-3	Sequence 3, Appl1	476	339	24.7	481	4	US-09-949-016-9238	Sequence 9238, Ap
404	343.5	25.0	460	6	5270178-13	Patent No. 5270178	477	339	24.7	481	4	US-09-949-016-9239	Sequence 9239, Ap
405	343.5	25.0	460	6	5270178-14	Patent No. 5270178	478	339	24.7	637	4	US-09-949-016-11538	Sequence 11538, A
406	343.5	25.0	460	6	5270178-15	Patent No. 5270178	479	339	24.7	637	4	US-09-949-016-11539	Sequence 11539, A
407	343.5	25.0	460	6	5270178-16	Patent No. 5270178	480	338.5	24.6	637	1	US-08-379-621-2	Sequence 2, Appl1
408	343.5	25.0	460	6	5270178-13	Patent No. 5270178	481	338.5	24.6	230	1	US-08-147-000B-2	Sequence 2, Appl1
409	343.5	25.0	460	6	5270178-14	Patent No. 5270178	482	338.5	24.6	230	2	US-08-147-000B-2	Sequence 2, Appl1
410	343.5	25.0	460	6	5270178-15	Patent No. 5270178	483	338.5	24.6	261	6	5270178-5	Patent No. 5270178
411	343.5	25.0	460	6	5270178-16	Patent No. 5270178	484	338.5	24.6	261	6	5270178-5	Patent No. 5270178
412	343	25.0	284	4	US-09-387-375-7	Sequence 7, Appl1	485	338.5	24.6	308	3	US-08-705-875A-10	Sequence 10, Appl
413	343	25.0	284	4	US-10-041-400A-7	Sequence 7, Appl1	486	338.5	24.6	308	4	US-09-242-999-10	Sequence 10, Appl
414	343	25.0	284	4	US-10-042-091A-7	Sequence 7, Appl1	487	338	24.6	250	3	US-08-944-483-51	Sequence 51, Appl
415	342.5	24.9	248	3	US-09-032-215-37	Sequence 37, Appl1	488	337.5	24.6	257	4	US-09-949-016-10711	Sequence 10711, A
416	342.5	24.9	249	3	US-09-079-970A-5	Sequence 5, Appl1	489	337	24.5	435	4	US-09-851-588-8	Sequence 8, Appl1
417	342.5	24.9	273	2	US-08-978-404B-6	Sequence 6, Appl1	490	337	24.5	435	4	US-09-851-588-8	Sequence 8, Appl1
418	342.5	24.9	546	6	5200340-6	Patent No. 5200340	491	337	24.5	435	4	US-09-607-745-2	Sequence 6, Appl1
419	342.5	24.9	546	6	5200340-6	Patent No. 5200340	492	337	24.5	435	4	US-09-607-745-2	Sequence 6, Appl1
420	342.5	24.9	713	4	US-09-949-016-9983	Sequence 9983, Ap	493	337	24.5	437	4	US-09-851-588-8	Sequence 8, Appl1
421	342.5	24.9	790	1	US-08-469-486-54	Sequence 54, Appl	494	337	24.5	437	4	US-08-248-629B-1	Sequence 1, Appl1
422	342.5	24.9	790	2	US-08-469-486-54	Sequence 54, Appl	495	337	24.5	812	1	US-08-451-932-1	Sequence 1, Appl1
423	342.5	24.9	791	2	US-09-131-995-1	Sequence 1, Appl1	496	337	24.5	812	1	US-08-451-932-1	Sequence 1, Appl1
424	342.5	24.9	791	2	US-08-832-087B-1	Sequence 1, Appl1	497	337	24.5	812	1	US-08-452-260-1	Sequence 1, Appl1
425	342.5	24.9	791	3	US-09-132-154-1	Sequence 1, Appl1	498	337	24.5	812	1	US-08-326-785-1	Sequence 1, Appl1
426	342.5	24.9	791	4	US-08-991-761A-6	Sequence 6, Appl1	499	337	24.5	812	2	US-08-612-788-1	Sequence 1, Appl1
427	342.5	24.9	810	1	US-08-924-287A-1	Sequence 1, Appl1	500	337	24.5	812	2	US-08-603-598B-1	Sequence 1, Appl1
428	342.5	24.9	810	1	US-07-854-603-2	Sequence 2, Appl1	501	337	24.5	812	2	US-08-429-743-1	Sequence 1, Appl1
429	342.5	24.9	810	1	US-08-147-000B-29	Sequence 29, Appl	502	337	24.5	812	2	US-08-866-735-1	Sequence 1, Appl1
430	342.5	24.9	810	3	US-09-086-514-1	Sequence 1, Appl1	503	337	24.5	812	3	US-09-066-028-1	Sequence 1, Appl1
431	342.5	24.9	810	4	US-09-192-012-5	Sequence 5, Appl1	504	337	24.5	812	4	US-09-192-012-3	Sequence 3, Appl1
432	342.5	24.9	810	4	US-09-403-736-1	Sequence 1, Appl1	505	337	24.5	812	4	US-09-135-325-1	Sequence 1, Appl1
433	342.5	24.9	810	4	US-09-701-265-1	Sequence 1, Appl1	506	337	24.5	812	4	US-08-991-761A-12	Sequence 12, Appl
434	342.5	24.9	810	6	5200340-8	Patent No. 5200340	507	336.5	24.5	812	5	PCT-US95-05107-1	Sequence 1, Appl1
435	342.5	24.9	810	6	5200340-8	Patent No. 5200340	508	336	24.5	415	3	US-09-008-271A-6	Sequence 6, Appl1
436	342	24.9	234	1	US-08-684-862-3	Sequence 3, Appl1	509	336	24.5	415	2	US-08-766-288-1	Sequence 1, Appl1
437	342	24.9	273	2	US-09-016-366A-19	Sequence 19, Appl	510	336	24.5	790	4	US-08-991-761A-13	Sequence 13, Appl
438	342	24.9	273	2	US-08-978-404B-14	Sequence 14, Appl	511	334.5	24.3	446	4	US-10-177-661-2	Sequence 4, Appl1
439	341.5	24.9	156	3	US-09-261-416-6	Sequence 6, Appl1	512	334.5	24.3	477	4	US-10-177-661-2	Sequence 4, Appl1
440	341.5	24.9	261	6	5270178-19	Patent No. 5270178	513	334.5	24.3	562	4	US-09-879-792-12	Sequence 12, Appl
441	341.5	24.9	261	6	5270178-20	Patent No. 5270178	514	334	24.3	316	4	US-09-387-375-9	Sequence 9, Appl1
442	341.5	24.9	261	6	5270178-19	Patent No. 5270178	515	334	24.3	316	4	US-10-041-400A-9	Sequence 9, Appl1
443	341.5	24.9	261	6	5270178-20	Patent No. 5270178	516	334	24.3	316	4	US-10-041-400A-9	Sequence 9, Appl1
444	341	24.8	261	6	5270178-21	Patent No. 5270178	517	333.5	24.3	290	4	US-09-386-653A-7	Sequence 7, Appl1
445	341	24.8	261	6	5270178-21	Patent No. 5270178	518	333.5	24.3	302	3	US-09-220-731-26	Sequence 26, Appl
446	341	24.8	306	4	US-09-386-642-53	Sequence 53, Appl	519	333.5	24.3	302	4	US-09-242-999-22	Sequence 22, Appl
447	341	24.8	415	4	US-09-118-748-2	Sequence 2, Appl1	520	333	24.2	415	1	US-08-295-471-2	Sequence 2, Appl1
448	340.5	24.8	230	1	US-08-456-840-47	Sequence 47, Appl	521	333	24.2	415	1	US-08-955-471-2	Sequence 2, Appl1
449	340.5	24.8	230	1	US-08-266-407A-47	Sequence 47, Appl	522	333	24.2	415	5	PCT-US92-10242-2	Sequence 2, Appl1
450	340.5	24.8	230	2	US-08-892-544-47	Sequence 47, Appl	523	332.5	24.2	638	5	US-08-681-151-3	Sequence 3, Appl1
451	340.5	24.8	230	3	US-08-766-982-12	Sequence 12, Appl	524	332.5	24.2	810	4	US-08-991-761A-11	Sequence 11, Appl
452	340.5	24.8	230	3	US-08-944-483-53	Sequence 53, Appl	525	331	24.1	295	3	US-08-338-368-2	Sequence 3, Appl1
453	340.5	24.8	230	3	US-09-296-219-12	Sequence 12, Appl	526	331	24.1	579	1	US-08-338-368-2	Sequence 3, Appl1
454	340.5	24.8	244	4	US-09-601-318-4	Sequence 4, Appl1	527	331	24.1	579	2	US-08-955-471-4	Sequence 4, Appl1
455	340.5	24.8	244	4	US-09-601-318-5	Sequence 5, Appl1	528	331	24.1	579	3	US-09-117-708-14	Sequence 14, Appl
456	340.5	24.8	244	4	US-09-601-318-6	Sequence 6, Appl1	529	331	24.1	579	5	PCT-US92-10242-3	Sequence 4, Appl1
457	340.5	24.8	244	4	US-09-601-318-7	Sequence 7, Appl1	530	331	24.1	615	1	US-07-998-972A-3	Sequence 3, Appl1
458	340.5	24.8	245	3	US-09-079-970A-6	Sequence 6, Appl1	531	331	24.1	615	1	US-08-462-953-3	Sequence 3, Appl1
459	340.5	24.8	245	3	US-09-601-318-1	Sequence 1, Appl1	532	331	24.1	615	1	US-08-462-261-3	Sequence 3, Appl1
460	340.5	24.8	267	2	US-09-016-366A-23	Sequence 23, Appl	533	331	24.1	615	5	PCT-US92-11357-3	Sequence 3, Appl1
461	340.5	24.8	267	4	US-08-978-404B-18	Sequence 18, Appl	534	331	24.1	622	4	US-08-958-967-8	Sequence 8, Appl1
462	340.5	24.8	267	4	US-09-917-254-101	Sequence 101, App	535	331	24.1	622	4	US-09-054-272-42	Sequence 42, Appl
463	340.5	24.8	300	3	US-08-705-875A-6	Sequence 6, Appl1	536	330.5	24.1	560	4	US-09-949-016-458	Sequence 6458, Ap
464	340.5	24.8	300	3	US-09-242-999-6	Sequence 6, Appl1	537	330.5	24.1	560	4	US-09-949-016-458	Sequence 3, Appl1
465	340	24.7	419	4	US-10-182-263-3	Sequence 3, Appl1	538	330	24.0	221	3	US-08-944-483-54	Sequence 54, Appl

539	330	24.0	222	1	US-08-456-840-46	Sequence 46, Appl	612	321	23.4	300	1	US-08-448-937A-1	Sequence 1, Appl
540	330	24.0	222	1	US-08-266-407A-46	Sequence 46, Appl	613	321	23.4	315	4	US-09-386-653A-9	Sequence 9, Appl
541	330	24.0	222	2	US-08-892-544-46	Sequence 46, Appl	614	321	23.4	655	1	US-08-148-910-12	Sequence 12, Appl
542	330	24.0	222	6	5223425-6	Patent No. 5223425	615	321	23.4	655	1	US-08-448-937A-12	Sequence 12, Appl
543	330	24.0	222	6	5223425-6	Patent No. 5223425	616	321	23.4	809	4	US-08-991-761A-9	Sequence 9, Appl
544	329.5	24.0	230	4	US-09-601-318-3	Sequence 3, Appl	617	319.5	23.3	240	1	US-08-278-091-11	Sequence 11, Appl
545	329.5	24.0	376	2	US-08-558-269-10	Sequence 10, Appl	618	319.5	23.3	240	1	US-08-483-859-11	Sequence 11, Appl
546	329.5	24.0	376	3	US-09-410-882-10	Sequence 10, Appl	619	319.5	23.3	240	1	US-08-472-173-11	Sequence 11, Appl
547	329	23.9	259	3	US-08-944-483-52	Sequence 52, Appl	620	319.5	23.3	240	2	US-08-487-167-11	Sequence 11, Appl
548	328.5	23.9	338	3	US-08-944-483-64	Sequence 64, Appl	621	319.5	23.3	240	2	US-08-482-816-11	Sequence 11, Appl
549	328.5	23.9	338	4	US-08-991-761A-10	Sequence 10, Appl	622	319.5	23.3	240	2	US-08-296-149-11	Sequence 11, Appl
550	327.5	23.8	151	3	US-09-518-046-21	Sequence 21, Appl	623	319.5	23.3	240	2	US-08-801-499-11	Sequence 11, Appl
551	327.5	23.8	151	3	US-09-261-416-7	Sequence 7, Appl	624	319.5	23.3	240	2	US-08-615-271-11	Sequence 11, Appl
552	327	23.8	241	3	US-08-944-483-60	Sequence 60, Appl	625	319.5	23.3	240	3	US-09-074-660-11	Sequence 11, Appl
553	327	23.8	255	1	US-08-650-129-5	Sequence 5, Appl	626	319.5	23.3	240	3	US-09-074-659-11	Sequence 11, Appl
554	327	23.8	255	1	US-08-984-417-5	Sequence 5, Appl	627	319.5	23.3	240	3	US-09-106-468-11	Sequence 11, Appl
555	326.5	23.8	144	4	US-09-618-259-1	Sequence 1, Appl	628	319.5	23.3	240	3	US-09-106-466A-11	Sequence 11, Appl
556	325.5	23.7	261	3	US-08-618-919A-2	Sequence 2, Appl	629	319.5	23.3	240	3	US-09-106-467-11	Sequence 11, Appl
557	325.5	23.7	261	4	US-08-462-515-2	Sequence 2, Appl	630	319.5	23.3	254	3	US-08-944-483-50	Sequence 50, Appl
558	325.5	23.7	261	5	PCT-US94-14073-2	Sequence 2, Appl	631	318	23.1	295	4	US-10-165-442-3	Sequence 3, Appl
559	325	23.7	226	1	US-08-650-129-4	Sequence 4, Appl	632	317.5	23.1	245	3	US-08-944-483-59	Sequence 69, Appl
560	325	23.7	226	1	US-08-984-417-4	Sequence 4, Appl	633	317	23.1	232	3	US-08-944-483-45	Sequence 45, Appl
561	324.5	23.6	228	1	US-08-278-091-10	Sequence 10, Appl	634	317	23.1	295	4	US-10-165-442-1	Sequence 1, Appl
562	324.5	23.6	228	1	US-08-483-859-10	Sequence 10, Appl	635	316.5	23.0	226	1	US-07-929-198-2	Sequence 2, Appl
563	324.5	23.6	228	1	US-08-472-173-10	Sequence 10, Appl	636	316.5	23.0	226	1	US-07-929-198-6	Sequence 6, Appl
564	324.5	23.6	228	2	US-08-487-167-10	Sequence 10, Appl	637	316.5	23.0	226	2	US-08-557-146-15	Sequence 15, Appl
565	324.5	23.6	228	2	US-08-482-816-10	Sequence 10, Appl	638	316.5	23.0	226	2	US-09-154-344-15	Sequence 15, Appl
566	324.5	23.6	228	2	US-08-296-149-10	Sequence 10, Appl	639	316.5	23.0	226	3	US-08-944-483-43	Sequence 43, Appl
567	324.5	23.6	228	2	US-08-801-499-10	Sequence 10, Appl	640	316	23.0	246	3	US-08-906-769-127	Sequence 127, App
568	324.5	23.6	228	2	US-08-615-271-10	Sequence 10, Appl	641	316	23.0	246	3	US-08-906-616-127	Sequence 127, App
569	324.5	23.6	228	3	US-09-074-660-10	Sequence 10, Appl	642	316	23.0	246	3	US-08-639-075A-127	Sequence 127, App
570	324.5	23.6	228	3	US-09-074-659-10	Sequence 10, Appl	643	316	23.0	246	3	US-09-012-431-127	Sequence 127, App
571	324.5	23.6	228	3	US-09-106-468-10	Sequence 10, Appl	644	316	23.0	246	3	US-09-012-632-127	Sequence 127, App
572	324.5	23.6	228	3	US-09-106-466A-10	Sequence 10, Appl	645	316	23.0	246	3	US-08-906-613-127	Sequence 127, App
573	324.5	23.6	228	3	US-09-106-467-10	Sequence 10, Appl	646	316	23.0	259	4	US-10-165-442-4	Sequence 4, Appl
574	323.5	23.5	275	2	US-09-016-366A-12	Sequence 12, Appl	647	315.5	23.0	254	3	US-09-578-303-5	Sequence 5, Appl
575	323.5	23.5	275	2	US-08-978-404B-17	Sequence 17, Appl	648	315.5	23.0	292	4	US-09-607-745-9	Sequence 9, Appl
576	323.5	23.5	406	1	US-08-293-778-24	Sequence 24, Appl	649	315.5	23.0	300	3	US-08-705-875A-4	Sequence 4, Appl
577	323.5	23.5	406	1	US-08-293-411-5	Sequence 5, Appl	650	315.5	23.0	300	3	US-09-220-731-21	Sequence 21, Appl
578	323.5	23.5	406	2	US-08-955-471-5	Sequence 5, Appl	651	315.5	23.0	300	4	US-09-242-999-4	Sequence 4, Appl
579	323.5	23.5	406	4	US-09-782-587B-1	Sequence 1, Appl	652	315.5	23.0	487	1	US-08-469-486-53	Sequence 53, Appl
580	323.5	23.5	406	4	US-09-782-587B-3	Sequence 3, Appl	653	315.5	23.0	487	2	US-08-469-658-53	Sequence 53, Appl
581	323.5	23.5	406	5	PCT-US92-10242-5	Sequence 5, Appl	654	315.5	23.0	492	1	US-08-469-486-2	Sequence 2, Appl
582	323.5	23.5	444	1	US-08-475-845-2	Sequence 2, Appl	655	315.5	23.0	492	2	US-08-469-658-2	Sequence 2, Appl
583	323.5	23.5	444	1	US-08-327-630-2	Sequence 2, Appl	656	315	22.9	259	4	US-10-165-442-5	Sequence 2, Appl
584	323.5	23.5	444	2	US-08-660-289-2	Sequence 2, Appl	657	315	22.9	691	4	US-09-949-011-775	Sequence 775, App
585	323.5	23.5	444	2	US-08-537-807-2	Sequence 2, Appl	658	314.5	22.9	855	4	US-09-244-111-2	Sequence 2, Appl
586	323.5	23.5	444	2	US-08-871-003-2	Sequence 2, Appl	659	314	22.9	855	2	US-09-027-337-2	Sequence 2, Appl
587	323.5	23.5	444	3	US-08-464-233-2	Sequence 2, Appl	660	314	22.9	855	4	US-09-644-600-2	Sequence 2, Appl
588	323.5	23.5	444	3	US-09-189-607-2	Sequence 2, Appl	661	314	22.9	855	4	US-09-654-600A-2	Sequence 2, Appl
589	323.5	23.5	444	3	US-09-378-907-2	Sequence 2, Appl	662	313.5	22.8	226	1	US-07-929-198-4	Sequence 4, Appl
590	323.5	23.5	444	5	PCT-US94-05779-2	Sequence 2, Appl	663	312.5	22.7	242	4	US-09-959-392-34	Sequence 34, Appl
591	323.5	23.5	461	4	US-09-949-016-8839	Sequence 8839, App	664	312	22.7	248	3	US-08-944-483-11	Sequence 71, Appl
592	323.5	23.5	466	1	US-07-882-202A-4	Sequence 4, Appl	665	311.5	22.7	251	3	US-08-944-483-17	Sequence 47, Appl
593	323.5	23.5	466	1	US-08-021-615A-4	Sequence 4, Appl	666	311	22.6	383	2	US-08-558-269-6	Sequence 6, Appl
594	323.5	23.5	466	1	US-08-321-777-4	Sequence 4, Appl	667	311	22.6	383	3	US-08-410-882-5	Sequence 6, Appl
595	323.5	23.5	466	1	US-09-009-217-14	Sequence 14, Appl	668	311	22.6	798	1	US-08-200-800A-2	Sequence 2, Appl
596	323.5	23.5	466	5	PCT-US93-04493-4	Sequence 4, Appl	669	311	22.6	798	5	US-08-794-042-2	Sequence 2, Appl
597	323.5	23.5	466	5	PCT-US93-04493-4	Sequence 4, Appl	670	311	22.6	798	5	PCT-US94-00616-2	Sequence 2, Appl
598	323.5	23.5	483	4	US-09-949-016-9523	Sequence 9523, App	671	311	22.6	812	4	US-09-192-012-9	Sequence 9, Appl
599	322.5	23.5	285	4	US-09-023-942A-26	Sequence 26, Appl	672	311	22.6	1042	4	US-09-959-392-2	Sequence 2, Appl
600	322.5	23.5	560	4	US-09-912-559-4	Sequence 4, Appl	673	310.5	22.6	247	2	US-08-978-404B-47	Sequence 47, Appl
601	322	23.4	207	4	US-10-000-469-54	Sequence 54, Appl	674	309.5	22.5	241	4	US-09-657-986B-2	Sequence 2, Appl
602	322	23.4	699	4	US-09-949-016-6138	Sequence 6138, App	675	309.5	22.5	492	4	US-09-665-166A-895	Sequence 895, App
603	322	23.4	717	4	US-09-949-016-11182	Sequence 11182, A	676	309.5	22.5	492	4	US-09-879-792-14	Sequence 14, Appl
604	321.5	23.4	255	2	US-09-027-337-7	Sequence 7, Appl	677	309.5	22.5	492	4	US-09-679-426-895	Sequence 895, App
605	321.5	23.4	255	4	US-09-644-600-7	Sequence 7, Appl	678	309.5	22.5	492	3	US-09-759-143-895	Sequence 895, App
606	321.5	23.4	255	4	US-09-654-600A-7	Sequence 7, Appl	679	308.5	22.5	243	3	US-08-944-483-70	Sequence 70, Appl
607	321.5	23.4	418	4	US-10-177-661-6	Sequence 6, Appl	680	308.5	22.5	319	4	US-09-270-767-42672	Sequence 42672, A
608	321	23.4	248	2	US-08-851-974-3	Sequence 3, Appl	681	308	22.4	317	4	US-09-959-392-32	Sequence 32, Appl
609	321	23.4	248	2	US-09-213-390-3	Sequence 3, Appl	682	308	22.4	317	4	US-09-386-629-7	Sequence 7, Appl
610	321	23.4	269	2	US-08-978-404B-10	Sequence 10, Appl	683	308	22.4	317	4	US-09-907-794A-263	Sequence 263, App
611	321	23.4	300	1	US-08-148-910-1	Sequence 1, Appl	684	308	22.4	317	4	US-09-905-125A-263	Sequence 263, App

685	308	22.4	317	4	US-09-902-775A-263	Sequence 263, App	758	304	22.1	562	6	5185259-3	Patent No. 5185259
686	308	22.4	317	4	US-09-906-700-263	Sequence 263, App	759	304	22.1	562	6	5200340-2	Patent No. 5200340
687	308	22.4	317	4	US-09-903-603A-263	Sequence 263, App	760	304	22.1	562	6	5244676-5	Patent No. 5244676
688	308	22.4	317	4	US-09-904-920A-263	Sequence 263, App	761	304	22.1	562	6	5344773-2	Patent No. 5344773
689	308	22.4	317	4	US-09-909-064-263	Sequence 263, App	762	304	22.1	562	6	5185259-3	Patent No. 5185259
690	308	22.4	317	4	US-09-905-381A-263	Sequence 263, App	763	304	22.1	562	6	5200340-2	Patent No. 5200340
691	308	22.4	317	4	US-09-906-618-263	Sequence 263, App	764	304	22.1	562	6	5244676-5	Patent No. 5244676
692	308	22.4	317	4	US-08-681-151-1	Sequence 1, Appl	765	304	22.1	562	6	5344773-2	Patent No. 5344773
693	307.5	22.3	376	4	US-09-820-002-2	Sequence 2, Appl	766	304	22.1	562	6	US-09-949-016-11501	Sequence 11501, A
694	307	22.3	268	1	US-08-568-031-2	Sequence 2, Appl	767	303.5	22.1	234	4	US-09-513-999C-7815	Sequence 7815, Ap
695	307	22.3	268	1	US-08-966-319-2	Sequence 2, Appl	768	303.5	22.1	278	1	US-08-392-828C-4	Sequence 4, Appl
696	307	22.3	355	2	US-09-153-304-2	Sequence 2, Appl	769	303.5	22.1	278	1	US-09-330-945-4	Sequence 4, Appl
697	307	22.3	355	2	US-08-811-949-47	Sequence 47, Appl	770	303	22.1	258	4	US-09-949-016-10661	Sequence 10661, A
698	307	22.3	355	2	US-08-811-949-59	Sequence 59, Appl	771	303	22.1	355	2	US-08-811-949-53	Sequence 53, Appl
699	307	22.3	417	4	US-08-820-002-4	Sequence 41, Appl	772	303	22.1	389	2	US-08-811-949-67	Sequence 67, Appl
700	307	22.3	437	2	US-08-811-949-51	Sequence 51, Appl	773	303	22.1	437	2	US-08-811-949-55	Sequence 55, Appl
701	307	22.3	452	4	US-09-949-016-7182	Sequence 7182, Ap	774	303	22.1	527	4	US-09-600-985-1	Sequence 1, Appl
702	307	22.3	527	4	US-08-811-949-39	Sequence 39, Appl	775	302.5	22.0	1113	4	US-09-959-392-4	Sequence 4, Appl
703	306	22.3	256	4	US-09-027-337-3	Sequence 3, Appl	776	302	22.0	477	2	US-08-811-949-65	Sequence 65, Appl
704	306	22.3	256	4	US-09-644-600-3	Sequence 3, Appl	777	302	22.0	477	2	US-08-811-949-51	Sequence 51, Appl
705	306	22.3	256	4	US-09-654-600A-3	Sequence 3, Appl	778	302	22.0	527	4	US-09-600-985-2	Sequence 2, Appl
706	306	22.3	437	2	US-08-811-949-57	Sequence 57, Appl	779	302	22.0	527	4	US-09-600-985-3	Sequence 3, Appl
707	305.5	22.2	146	4	US-09-618-259-3	Sequence 3, Appl	780	301.5	21.9	226	3	US-08-944-483-41	Sequence 41, Appl
708	305	22.2	247	2	US-08-851-974-1	Sequence 1, Appl	781	301	21.9	255	1	US-08-208-007A-14	Sequence 14, Appl
709	305	22.2	247	2	US-08-851-974-4	Sequence 4, Appl	782	301	21.9	255	3	US-08-915-095A-14	Sequence 14, Appl
710	305	22.2	247	2	US-09-213-390-1	Sequence 1, Appl	783	301	21.9	255	3	US-08-798-096-14	Sequence 14, Appl
711	305	22.2	247	2	US-09-213-390-4	Sequence 4, Appl	784	301	21.9	255	4	US-08-798-095A-14	Sequence 14, Appl
712	305	22.2	247	2	US-09-949-016-6457	Sequence 6457, Ap	785	301	21.9	255	4	US-09-953-956-14	Sequence 14, Appl
713	305	22.2	437	2	US-08-811-949-64	Sequence 49, Appl	786	301	21.9	255	4	US-08-553-125A-14	Sequence 14, Appl
714	304.5	22.2	258	3	US-09-004-731-16	Sequence 16, Appl	787	301	21.9	257	4	US-10-114-464-14	Sequence 14, Appl
715	304.5	22.2	258	3	US-09-004-731-16	Sequence 16, Appl	788	301	21.9	527	6	5520913-1	Patent No. 5520913
716	304.5	22.2	258	3	US-09-004-731-16	Sequence 16, Appl	789	301	21.9	527	6	5520913-1	Patent No. 5520913
717	304.5	22.2	258	3	US-08-749-699-16	Sequence 19, Appl	790	301	21.9	527	6	5520913-1	Patent No. 5520913
718	304.5	22.2	258	4	US-08-749-699-19	Sequence 19, Appl	791	300	21.8	233	4	US-09-636-382A-24	Sequence 24, Appl
719	304.5	22.2	258	4	US-09-004-729-16	Sequence 16, Appl	792	298	21.7	347	2	US-08-811-949-1	Sequence 1, Appl
720	304.5	22.2	384	4	US-09-004-729-19	Sequence 22, Appl	793	297	21.6	237	3	US-08-163-919A-3	Sequence 3, Appl
721	304.5	22.2	384	3	US-09-032-215-22	Sequence 22, Appl	794	297	21.6	237	3	US-08-462-515-3	Sequence 3, Appl
722	304.5	22.2	393	4	US-09-759-143-934	Sequence 934, App	795	297	21.6	237	5	PCT-US94-14073-3	Sequence 3, Appl
723	304.5	22.2	492	3	US-09-342-749-2	Sequence 2, Appl	796	297	21.6	237	5	US-08-944-483-72	Sequence 72, Appl
724	304.5	22.2	492	4	US-09-691-840-2	Sequence 2, Appl	797	297	21.6	252	3	US-09-027-337-8	Sequence 8, Appl
725	304.5	22.2	510	4	US-09-759-143-932	Sequence 932, App	798	297	21.6	253	2	US-09-027-337-8	Sequence 8, Appl
726	304.5	22.2	510	4	US-09-949-016-11074	Sequence 11074, A	799	297	21.6	253	4	US-09-644-600-8	Sequence 8, Appl
727	304	22.1	232	1	US-07-990-301A-4	Sequence 4, Appl	799	297	21.6	253	4	US-09-654-600A-8	Sequence 8, Appl
728	304	22.1	235	3	US-08-944-483-65	Sequence 65, Appl	799	297	21.6	253	4	US-09-654-600A-8	Sequence 8, Appl
729	304	22.1	235	3	US-08-944-483-65	Sequence 65, Appl	800	297	21.6	253	4	US-09-654-600A-8	Sequence 8, Appl
730	304	22.1	268	4	US-09-613-822B-2	Sequence 2, Appl	801	297	21.6	323	4	US-09-032-215-27	Sequence 27, Appl
731	304	22.1	327	4	US-09-386-629-8	Sequence 8, Appl	802	297	21.6	354	2	US-08-811-949-61	Sequence 61, Appl
732	304	22.1	355	1	US-08-137-116-1	Sequence 1, Appl	803	297	21.6	411	3	US-09-949-016-11081	Sequence 11081, A
733	304	22.1	355	1	US-08-217-618-1	Sequence 1, Appl	804	297	21.6	521	4	US-09-949-016-11082	Sequence 11082, A
734	304	22.1	355	1	US-08-427-640-2	Sequence 2, Appl	806	297	21.6	521	4	US-09-949-016-11083	Sequence 11083, A
735	304	22.1	355	1	US-08-427-640-6	Sequence 6, Appl	807	296.5	21.6	224	1	US-08-483-859-12	Sequence 12, Appl
736	304	22.1	355	1	US-08-217-617A-1	Sequence 1, Appl	808	296.5	21.6	224	1	US-08-487-167-12	Sequence 12, Appl
737	304	22.1	355	1	US-08-217-617A-1	Sequence 1, Appl	809	296.5	21.6	224	1	US-08-487-167-12	Sequence 12, Appl
738	304	22.1	355	2	US-08-811-949-45	Sequence 45, Appl	810	296.5	21.6	224	2	US-08-487-167-12	Sequence 12, Appl
739	304	22.1	355	2	US-08-811-949-45	Sequence 45, Appl	811	296.5	21.6	224	2	US-08-487-167-12	Sequence 12, Appl
740	304	22.1	355	6	US-08-794-528-1	Sequence 1, Appl	812	296.5	21.6	224	2	US-08-296-149-12	Sequence 12, Appl
741	304	22.1	355	6	5223256-1	Patent No. 5223256	813	296.5	21.6	224	2	US-08-296-149-12	Sequence 12, Appl
742	304	22.1	356	1	US-08-427-640-4	Sequence 4, Appl	814	296.5	21.6	224	2	US-08-801-499-12	Sequence 12, Appl
743	304	22.1	356	1	US-08-427-640-8	Sequence 8, Appl	815	296.5	21.6	224	2	US-08-615-271-12	Sequence 12, Appl
744	304	22.1	378	3	US-09-553-498-10	Sequence 10, Appl	816	296.5	21.6	224	3	US-09-074-660-12	Sequence 12, Appl
745	304	22.1	378	4	US-09-618-869-10	Sequence 10, Appl	817	296.5	21.6	224	3	US-09-074-660-12	Sequence 12, Appl
746	304	22.1	433	4	US-09-949-016-8220	Sequence 8220, Ap	818	296.5	21.6	224	3	US-09-106-468-12	Sequence 12, Appl
747	304	22.1	472	1	US-08-811-949-63	Sequence 63, Appl	819	296.5	21.6	224	3	US-09-106-468-12	Sequence 12, Appl
748	304	22.1	527	1	US-07-609-510B-16	Sequence 16, Appl	820	296.5	21.6	224	3	US-09-106-468-12	Sequence 12, Appl
749	304	22.1	527	4	US-09-612-314A-51	Sequence 51, Appl	821	296.5	21.6	254	4	US-09-106-467-12	Sequence 12, Appl
750	304	22.1	527	5	PCT-US91-01025A-2	Sequence 2, Appl	822	296.5	21.6	254	4	US-09-205-258-1149	Sequence 1149, Ap
751	304	22.1	527	6	5185259-8	Patent No. 5185259	823	296.5	21.6	276	4	US-09-880-503-5	Sequence 49, Appl
752	304	22.1	527	6	5185259-8	Patent No. 5185259	824	296.5	21.6	306	2	US-08-560-098A-45	Sequence 45, Appl
753	304	22.1	562	2	US-08-811-949-43	Sequence 43, Appl	825	296.5	21.6	331	2	US-08-560-098A-46	Sequence 46, Appl
754	304	22.1	562	2	US-08-560-098A-50	Sequence 50, Appl	826	296.5	21.6	365	1	US-08-093-741-93	Sequence 83, Appl
755	304	22.1	562	2	US-08-883-795A-38	Sequence 38, Appl	827	296.5	21.6	365	1	US-08-720-012-83	Sequence 84, Appl
756	304	22.1	562	4	US-09-703-695A-4	Sequence 4, Appl	828	296.5	21.6	393	3	US-08-560-098A-44	Sequence 44, Appl
757	304	22.1	562	4	US-10-443-701-4	Sequence 4, Appl	829	296.5	21.6	393	3	US-08-967-024C-24	Sequence 24, Appl
							830	296.5	21.6	403	4	US-08-967-024C-25	Sequence 25, Appl
												US-09-880-503-6	Sequence 6, Appl

831	296.5	21.6	411	1	US-08-087-163-1	Sequence 1, Appl1	904	282	20.5	244	3	US-08-944-483-74	Sequence 74, Appl1
832	296.5	21.6	411	1	US-08-286-748B-18	Sequence 18, Appl1	905	279	20.3	902	4	US-09-644-600-10	Sequence 10, Appl1
833	296.5	21.6	411	1	US-08-153-799-18	Sequence 18, Appl1	906	279	20.3	902	4	US-09-654-600A-10	Sequence 10, Appl1
834	296.5	21.6	411	2	US-08-560-098A-48	Sequence 48, Appl1	907	277.5	20.2	242	3	US-08-944-483-58	Sequence 58, Appl1
835	296.5	21.6	411	4	US-09-880-503-3	Sequence 3, Appl1	908	277	20.2	488	4	US-09-367-777-44	Sequence 44, Appl1
836	296.5	21.6	430	6	5219569-2	Patent No. 5219569	909	277	20.2	488	4	US-09-367-791A-27	Sequence 27, Appl1
837	296.5	21.6	430	6	5219569-2	Patent No. 5219569	910	276	20.1	306	1	US-08-330-978-1	Sequence 1, Appl1
838	296.5	21.6	431	4	US-09-101-272G-1	Sequence 1, Appl1	911	276	20.1	306	1	US-08-474-042-1	Sequence 1, Appl1
839	296.5	21.6	431	6	5188829-1	Patent No. 5188829	912	276	20.1	306	1	US-08-484-558-1	Sequence 1, Appl1
840	296.5	21.6	431	6	5188829-1	Patent No. 5188829	913	276	20.1	306	1	US-08-774-592-1	Sequence 1, Appl1
841	296.5	21.6	432	6	US-08-560-098A-47	Sequence 47, Appl1	914	276	20.1	437	1	US-08-487-037-2	Sequence 2, Appl1
842	296.5	21.5	269	4	US-09-715-994-2	Sequence 2, Appl1	915	276	20.1	448	1	US-08-295-411-3	Sequence 3, Appl1
843	295.5	21.5	283	3	US-08-807-151-1	Sequence 1, Appl1	916	276	20.1	448	2	US-08-955-471-3	Sequence 3, Appl1
844	295.5	21.5	283	3	US-09-478-957-1	Sequence 1, Appl1	917	276	20.1	448	5	PCT-US97-10242-3	Sequence 1, Appl1
845	295.5	21.5	454	3	US-09-518-066-2	Sequence 2, Appl1	918	276	20.1	448	5	PCT-US97-10242-3	Sequence 1, Appl1
846	294	21.4	256	3	US-09-032-215-22	Sequence 3, Appl1	919	276	20.1	488	1	US-08-467-037-1	Sequence 1, Appl1
847	293.5	21.4	239	3	US-08-944-483-61	Sequence 61, Appl1	920	276	20.1	464	4	US-09-949-016-9524	Sequence 9524, Ap
848	293.5	21.4	411	4	US-09-403-736-2	Sequence 2, Appl1	921	274.5	20.0	211	3	US-09-220-731-25	Sequence 25, Appl1
849	293.5	21.4	430	1	US-07-942-157A-3	Sequence 3, Appl1	922	274.5	20.0	211	4	US-09-242-999-20	Sequence 20, Appl1
850	292	21.3	237	3	US-09-004-731-22	Sequence 22, Appl1	923	274	19.9	241	1	US-08-330-978-4	Sequence 4, Appl1
851	292	21.3	237	3	US-08-749-699-22	Sequence 22, Appl1	924	274	19.9	241	1	US-08-474-042-4	Sequence 4, Appl1
852	292	21.3	237	4	US-09-004-729-22	Sequence 22, Appl1	925	274	19.9	241	1	US-08-484-558-4	Sequence 4, Appl1
853	292	21.3	256	3	US-08-906-769-89	Sequence 89, Appl1	926	274	19.9	241	1	US-08-774-592-4	Sequence 4, Appl1
854	292	21.3	256	3	US-08-906-616-89	Sequence 89, Appl1	927	274	19.9	254	1	US-08-330-978-3	Sequence 3, Appl1
855	292	21.3	256	3	US-08-817-795-89	Sequence 89, Appl1	928	274	19.9	254	1	US-08-474-042-3	Sequence 3, Appl1
856	292	21.3	256	3	US-08-639-075A-89	Sequence 89, Appl1	929	274	19.9	254	1	US-08-484-558-3	Sequence 3, Appl1
857	292	21.3	256	3	US-09-012-431-59	Sequence 89, Appl1	930	274	19.9	254	1	US-08-774-592-3	Sequence 3, Appl1
858	292	21.3	256	3	US-09-012-692-89	Sequence 89, Appl1	931	272	19.8	253	3	US-08-906-769-131	Sequence 11, App
859	292	21.3	256	3	US-08-906-613-89	Sequence 89, Appl1	932	272	19.8	253	3	US-08-906-616-131	Sequence 11, App
860	292	21.3	256	5	PCT-US95-14442A-89	Sequence 89, Appl1	933	272	19.8	253	3	US-08-639-075A-131	Sequence 11, App
861	292	21.3	414	4	US-09-270-767-6426	Sequence 48, Appl1	934	272	19.8	253	3	US-09-012-431-131	Sequence 11, App
862	291.5	21.2	242	3	US-08-944-483-57	Sequence 4626, A	935	272	19.8	253	3	US-09-012-692-131	Sequence 11, App
863	291.5	21.2	243	3	US-08-944-483-57	Sequence 57, Appl1	936	272	19.8	253	3	US-08-906-613-131	Sequence 11, App
864	291	21.2	243	3	US-08-944-483-57	Sequence 7, Appl1	937	272	19.8	251	3	US-08-944-483-28	Sequence 28, Appl1
865	290	21.1	235	2	US-09-000-846-2	Sequence 2, Appl1	938	270	19.7	251	3	US-08-944-483-28	Sequence 28, Appl1
866	290	21.1	235	2	US-08-557-146-14	Sequence 14, Appl1	939	269	19.6	256	4	US-08-395-456C-23	Sequence 23, Appl1
867	290	21.1	235	2	US-09-154-344-14	Sequence 14, Appl1	940	269	19.6	256	2	US-08-487-453A-23	Sequence 23, Appl1
868	290	21.1	235	3	US-08-807-151-3	Sequence 3, Appl1	941	268	19.5	256	2	US-08-230-428B-4	Sequence 4, Appl1
869	290	21.1	235	3	US-08-944-483-42	Sequence 42, Appl1	942	267.5	19.5	266	3	US-08-487-037-3	Sequence 3, Appl1
870	289	21.0	223	1	US-07-956-848A-41	Sequence 3, Appl1	943	267.5	19.5	266	3	US-09-004-731-24	Sequence 24, Appl1
871	289	21.0	223	1	US-08-471-956-41	Sequence 41, Appl1	944	267.5	19.5	266	3	US-08-749-699-24	Sequence 24, Appl1
872	289	21.0	583	4	US-09-976-594-837	Sequence 837, App	945	265.5	19.3	197	1	US-09-004-729-24	Sequence 24, Appl1
873	288.5	21.0	255	3	US-08-906-769-91	Sequence 91, Appl1	946	265.5	19.3	197	1	US-08-456-840-48	Sequence 48, Appl1
874	288.5	21.0	255	3	US-08-906-616-81	Sequence 91, Appl1	947	265.5	19.3	197	2	US-08-266-407A-48	Sequence 48, Appl1
875	288.5	21.0	255	3	US-08-817-795-91	Sequence 91, Appl1	948	264.5	19.3	248	1	US-08-238-130-2	Sequence 2, Appl1
876	288.5	21.0	255	3	US-08-639-075A-91	Sequence 91, Appl1	949	264.5	19.3	248	2	US-08-921-426-4	Sequence 2, Appl1
877	288.5	21.0	255	3	US-09-012-431-91	Sequence 91, Appl1	950	264.5	19.3	248	3	US-08-816-915-4	Sequence 4, Appl1
878	288.5	21.0	255	3	US-09-012-692-81	Sequence 91, Appl1	951	264.5	19.3	248	5	PCT-US95-07743-4	Sequence 4, Appl1
879	288.5	21.0	255	3	US-08-906-613-91	Sequence 91, Appl1	952	264.5	19.3	249	3	US-09-578-303-2	Sequence 2, Appl1
880	288.5	21.0	255	5	PCT-US95-14442A-91	Sequence 91, Appl1	953	264	19.2	260	3	US-08-944-483-68	Sequence 68, Appl1
881	288	21.0	268	1	US-08-270-584A-2	Sequence 2, Appl1	954	264	19.2	256	4	US-09-949-016-6271	Sequence 6271, Ap
882	288	21.0	268	2	US-08-765-192-2	Sequence 2, Appl1	955	263.5	19.2	222	2	US-08-491-204A-18	Sequence 18, Appl1
883	288	21.0	268	3	US-09-199-793-2	Sequence 2, Appl1	956	263.5	19.2	251	4	US-09-949-016-6112	Sequence 6112, Ap
884	287	20.9	227	3	US-08-944-483-0	Sequence 40, Appl1	957	263.5	19.2	255	4	US-09-949-016-9690	Sequence 9690, Ap
885	287	20.9	407	3	US-09-734-675-4	Sequence 4, Appl1	958	263	19.1	252	3	US-08-906-769-103	Sequence 103, App
886	286.5	20.9	218	3	US-09-578-303-3	Sequence 3, Appl1	959	263	19.1	252	3	US-08-906-616-103	Sequence 103, App
887	286.5	20.9	228	3	US-09-004-731-10	Sequence 10, Appl1	960	263	19.1	252	3	US-08-817-795-103	Sequence 103, App
888	286.5	20.9	228	3	US-08-749-699-10	Sequence 10, Appl1	961	263	19.1	252	3	US-08-639-075A-103	Sequence 103, App
889	286.5	20.9	228	4	US-09-004-729-10	Sequence 10, Appl1	962	263	19.1	252	3	US-09-012-431-103	Sequence 103, App
890	286	20.8	228	4	US-09-205-258-1150	Sequence 1150, Ap	963	263	19.1	252	3	US-09-012-692-103	Sequence 103, App
891	284.5	20.7	225	3	US-09-004-731-13	Sequence 13, Appl1	964	263	19.1	252	3	US-08-906-613-103	Sequence 103, App
892	284.5	20.7	225	3	US-08-749-699-13	Sequence 13, Appl1	965	263	19.1	252	5	PCT-US95-14442A-103	Sequence 103, App
893	284.5	20.7	225	4	US-09-004-729-13	Sequence 13, Appl1	966	262.5	19.1	253	3	US-09-004-731-27	Sequence 27, Appl1
894	284.5	20.7	225	3	US-08-906-769-83	Sequence 83, Appl1	967	262.5	19.1	253	3	US-08-749-699-27	Sequence 27, Appl1
895	284.5	20.7	225	3	US-08-906-616-83	Sequence 83, Appl1	968	262.5	19.1	253	4	US-09-004-729-27	Sequence 27, Appl1
896	284.5	20.7	225	3	US-08-817-795-83	Sequence 83, Appl1	969	261.5	19.0	222	1	US-07-969-931-9	Sequence 9, Appl1
897	284.5	20.7	225	3	US-08-639-075A-83	Sequence 83, Appl1	970	261.5	19.0	222	1	US-07-855-417A-9	Sequence 9, Appl1
898	284.5	20.7	225	3	US-09-012-431-83	Sequence 83, Appl1	971	261.5	18.7	225	3	US-08-944-483-32	Sequence 32, Appl1
899	284.5	20.7	225	3	US-09-012-692-83	Sequence 83, Appl1	972	257.5	18.7	224	1	US-08-553-516-2	Sequence 2, Appl1
900	284.5	20.7	225	3	US-08-906-613-83	Sequence 83, Appl1	973	256	18.6	267	3	US-08-906-769-145	Sequence 145, App
901	284.5	20.7	225	5	PCT-US95-14442A-83	Sequence 83, Appl1	974	256	18.6	267	3	US-08-906-616-145	Sequence 145, App
902	283.5	20.6	268	3	US-09-032-215-62	Sequence 42, Appl1	975	256	18.6	267	3	US-08-639-075A-145	Sequence 145, App
903	282.5	20.6	144	4	US-09-618-259-4	Sequence 4, Appl1	976	256	18.6	267	3	US-09-004-731-67	Sequence 67, Appl1

977	256	18.6	267	3	US-09-012-431-145	Sequence 145, App	1050	226	16.4	697	3	US-08-462-040-50	Sequence 50, Appl
978	256	18.6	267	3	US-08-749-699-67	Sequence 67, Appl	1051	226	16.4	723	1	US-07-838-410-1	Sequence 1, Appl
979	256	18.6	267	3	US-09-012-692-145	Sequence 145, App	1052	226	16.4	723	1	US-08-290-937B-1	Sequence 1, Appl
980	256	18.6	267	3	US-08-906-613-145	Sequence 145, App	1053	226	16.4	723	1	US-08-290-937B-2	Sequence 2, Appl
981	256	18.6	267	3	US-09-004-729-67	Sequence 67, Appl	1054	226	16.4	723	1	US-08-290-937B-3	Sequence 3, Appl
982	256	18.6	405	3	US-09-734-675-2	Sequence 2, Appl	1055	226	16.4	723	1	US-08-404-643-1	Sequence 1, Appl
983	254	18.5	242	3	US-09-004-731-41	Sequence 41, Appl	1056	226	16.4	723	1	US-09-194-326-1	Sequence 1, Appl
984	254	18.5	242	3	US-08-749-699-41	Sequence 41, Appl	1057	226	16.4	723	3	US-09-194-326-2	Sequence 2, Appl
985	254	18.5	242	4	US-09-004-729-41	Sequence 41, Appl	1058	226	16.4	723	3	US-09-194-326-3	Sequence 3, Appl
986	254	18.5	255	4	US-09-270-767-4461	Sequence 4461, A	1059	226	16.4	723	4	US-08-700-519J-19	Sequence 19, Appl
987	253	18.4	182	4	US-09-328-925-12	Sequence 12, Appl	1060	226	16.4	723	3	US-09-600-991-18	Sequence 18, Appl
988	253	18.4	231	4	US-08-395-456C-25	Sequence 25, Appl	1061	226	16.4	723	4	US-08-605-221-4	Sequence 4, Appl
989	253	18.4	242	3	US-09-032-215-47	Sequence 47, Appl	1062	226	16.4	723	4	US-07-815-333A-2	Sequence 2, Appl
990	252.5	18.4	221	2	US-08-925-708-1	Sequence 1, Appl	1063	226	16.4	728	1	US-08-807-783A-22	Sequence 22, Appl
991	252.5	18.4	239	3	US-09-004-731-44	Sequence 44, Appl	1064	226	16.4	728	1	US-08-605-221-2	Sequence 2, Appl
992	252.5	18.4	239	3	US-08-749-699-44	Sequence 44, Appl	1065	226	16.4	728	1	US-08-906-616-149	Sequence 149, App
993	252.5	18.4	239	3	US-09-004-729-44	Sequence 44, Appl	1066	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
994	252.5	18.4	247	3	US-08-944-483-49	Sequence 49, Appl	1067	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
995	252	18.3	229	2	US-08-395-456C-27	Sequence 27, Appl	1068	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
996	251	18.3	229	2	US-08-395-456C-20	Sequence 20, Appl	1069	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
997	251	18.3	229	4	US-08-487-453A-20	Sequence 20, Appl	1070	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
998	251	18.3	229	4	US-08-944-483-30	Sequence 30, Appl	1071	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
999	251	18.3	229	5	PCT-US95-02513-20	Sequence 20, Appl	1072	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
1000	250	18.2	352	4	US-09-902-540-9796	Sequence 9796, Ap	1073	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
1001	248.5	18.1	717	4	US-09-601-040A-6	Sequence 6, Appl	1074	220.5	16.0	267	2	US-08-978-404B-46	Sequence 46, Appl
1002	248.5	18.1	717	4	US-09-601-040A-2	Sequence 2, Appl	1075	220	16.0	278	4	US-09-270-767-48024	Sequence 48024, A
1003	247.5	18.0	719	4	US-09-601-040A-8	Sequence 8, Appl	1076	220	16.0	457	4	US-09-270-767-48024	Sequence 48024, A
1004	247.5	18.0	729	4	US-09-601-040A-4	Sequence 4, Appl	1077	217.5	15.8	385	4	US-09-163-951-16	Sequence 16, Appl
1005	247.5	18.0	229	3	US-08-944-483-30	Sequence 30, Appl	1078	217.5	15.8	385	4	US-09-163-951-16	Sequence 16, Appl
1006	245	17.8	226	4	US-09-601-040A-28	Sequence 28, Appl	1079	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1007	245	17.8	228	2	US-08-766-982-11	Sequence 11, Appl	1080	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1008	245	17.8	228	2	US-08-766-982-11	Sequence 11, Appl	1081	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1009	245	17.8	228	2	US-08-944-483-55	Sequence 55, Appl	1082	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1010	245	17.8	711	1	US-09-296-219-11	Sequence 11, Appl	1083	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1011	245	17.8	711	1	US-08-184-012C-8	Sequence 8, Appl	1084	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1012	245	17.8	711	2	US-08-334-177-2	Sequence 2, Appl	1085	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1013	245	17.8	711	2	US-08-666-082B-1	Sequence 1, Appl	1086	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1014	245	17.8	711	2	US-08-766-982-2	Sequence 2, Appl	1087	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1015	245	17.8	711	3	US-09-296-219-2	Sequence 2, Appl	1088	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1016	245	17.8	711	4	US-09-600-991-20	Sequence 20, Appl	1089	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1017	245	17.8	711	4	US-09-601-040A-12	Sequence 12, Appl	1090	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1018	244.5	17.8	711	5	US-09-949-016-6981	Sequence 6981, Ap	1091	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1019	244.5	17.8	716	2	PCT-US95-13830-2	Sequence 2, Appl	1092	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1020	244.5	17.8	716	2	US-08-766-982-1	Sequence 1, Appl	1093	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1021	242	17.6	214	6	US-09-296-219-1	Sequence 1, Appl	1094	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1022	242	17.6	214	6	5180819-3	Patent No. 5180819	1095	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1023	242	17.6	455	3	US-09-261-416-2	Sequence 2, Appl	1096	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1024	240	17.5	161	3	US-09-261-416-8	Sequence 8, Appl	1097	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1025	234	17.0	158	3	US-09-518-046-22	Sequence 22, Appl	1098	211	15.4	223	1	US-08-485-455D-17	Sequence 17, Appl
1026	232.5	16.9	185	3	US-08-705-875A-5	Sequence 5, Appl	1099	211	15.4	223	2	US-08-485-455D-17	Sequence 17, Appl
1027	232.5	16.9	185	3	US-08-705-875A-5	Sequence 5, Appl	1100	211	15.4	223	2	US-08-485-455D-17	Sequence 17, Appl
1028	232.5	16.9	185	3	US-08-705-875A-5	Sequence 5, Appl	1101	211	15.4	223	2	US-08-485-455D-17	Sequence 17, Appl
1029	231.5	16.8	185	4	US-09-220-731-22	Sequence 22, Appl	1102	211	15.4	223	3	US-08-485-455D-17	Sequence 17, Appl
1030	231	16.8	219	2	US-08-242-999-5	Sequence 5, Appl	1103	211	15.4	223	3	US-08-485-455D-17	Sequence 17, Appl
1031	230.5	16.8	304	3	US-08-925-708-2	Sequence 2, Appl	1104	211	15.4	223	3	US-08-485-455D-17	Sequence 17, Appl
1032	228.5	16.6	287	4	US-08-944-483-29	Sequence 29, Appl	1105	211	15.4	224	3	PCT-US95-14442A-17	Sequence 17, Appl
1033	228.5	16.6	287	4	US-09-088-651-1	Sequence 1, Appl	1106	211	15.4	224	3	US-08-906-616-17	Sequence 17, Appl
1034	227	16.5	258	4	US-09-270-767-33263	Sequence 33263, A	1107	211	15.4	224	3	US-08-906-616-17	Sequence 17, Appl
1035	227	16.5	258	4	US-09-023-942A-8	Sequence 8, Appl	1108	211	15.4	224	3	US-08-906-616-17	Sequence 17, Appl
1036	227	16.5	259	3	US-08-906-769-190	Sequence 190, App	1109	211	15.4	224	3	US-08-906-616-17	Sequence 17, Appl
1037	227	16.5	259	3	US-08-906-769-190	Sequence 190, App	1110	211	15.4	224	3	US-08-906-616-17	Sequence 17, Appl
1038	227	16.5	259	3	US-08-639-075A-190	Sequence 190, App	1111	211	15.4	224	3	US-08-906-616-17	Sequence 17, Appl
1039	227	16.5	259	3	US-09-004-731-85	Sequence 85, Appl	1112	210.5	15.3	228	4	US-08-906-616-17	Sequence 17, Appl
1040	227	16.5	259	3	US-09-012-431-190	Sequence 190, App	1113	210.5	15.3	228	4	US-08-906-616-17	Sequence 17, Appl
1041	227	16.5	259	3	US-08-749-699-85	Sequence 85, Appl	1114	210.5	15.3	228	4	US-08-906-616-17	Sequence 17, Appl
1042	227	16.5	259	3	US-09-012-692-190	Sequence 190, App	1115	206	15.0	164	3	US-09-518-046-25	Sequence 25, Appl
1043	227	16.5	259	4	US-08-906-613-190	Sequence 190, App	1116	206	15.0	164	3	US-09-518-046-25	Sequence 25, Appl
1044	227	16.5	723	3	US-09-004-729-85	Sequence 85, Appl	1117	204.5	14.9	157	4	US-08-518-046-23	Sequence 23, Appl
1045	226.5	16.5	215	6	US-08-700-519J-18	Sequence 18, Appl	1118	204.5	14.9	178	3	US-08-906-616-107	Sequence 107, App
1046	226.5	16.5	215	6	5180819-2	Patent No. 5180819	1119	204.5	14.9	178	3	US-08-906-616-107	Sequence 107, App
1047	226	16.4	697	3	5180819-2	Patent No. 5180819	1120	204.5	14.9	178	3	US-08-906-616-107	Sequence 107, App
1048	226	16.4	697	3	US-08-167-641C-50	Sequence 50, Appl	1121	204.5	14.9	178	3	US-08-906-616-107	Sequence 107, App
1049	226	16.4	697	3	US-08-460-971A-50	Sequence 50, Appl	1122	204.5	14.9	178	3	US-08-460-971A-50	Sequence 50, Appl

1123	204.5	14.9	178	3	US-09-012-692-107	Sequence 107, App	1196	160.5	11.7	178	3	US-09-220-731-24	Sequence 24, Appl
1124	204.5	14.9	178	3	US-08-906-613-107	Sequence 107, App	1197	160.5	11.7	178	4	US-09-242-999-24	Sequence 24, Appl
1125	204.5	14.9	178	5	PCT-US95-14442A-107	Sequence 107, App	1198	160	11.6	97	4	US-09-270-767-11931	Sequence 24, Appl
1126	200.5	14.6	159	3	US-09-518-046-24	Sequence 24, Appl	1199	160	11.6	97	4	US-09-270-767-47148	Sequence 47148, A
1127	200	14.6	223	4	US-09-270-767-45768	Sequence 45768, A	1200	159	11.6	190	2	US-08-845-998-6	Sequence 6, Appl1
1128	198.5	14.4	254	3	US-08-906-769-129	Sequence 129, App	1201	159	11.6	190	3	US-09-206-537-6	Sequence 6, Appl1
1129	198.5	14.4	254	3	US-08-906-616-129	Sequence 129, App	1202	159	11.6	190	3	US-09-430-854-6	Sequence 6, Appl1
1130	198.5	14.4	254	3	US-08-639-075A-129	Sequence 129, App	1203	158	11.5	357	4	US-09-270-767-43564	Sequence 43564, A
1131	198.5	14.4	254	3	US-09-012-431-129	Sequence 129, App	1204	158	11.5	357	4	US-09-270-767-48936	Sequence 58936, A
1132	198.5	14.4	254	3	US-09-012-692-129	Sequence 129, App	1205	157.5	11.5	764	2	US-08-177-109A-2	Sequence 2, Appl1
1133	198.5	14.4	254	3	US-08-906-613-129	Sequence 129, App	1206	157.5	11.5	764	2	US-08-687-706-2	Sequence 2, Appl1
1134	196.5	14.3	326	4	US-09-949-016-7265	Sequence 7265, App	1207	157.5	11.5	798	4	US-09-949-016-11021	Sequence 11021, App
1135	195	14.2	326	4	US-09-411-977-3	Sequence 3, Appl1	1208	157	11.4	141	4	US-09-513-999C-4215	Sequence 4215, App
1136	195	14.2	326	4	US-10-057-951-3	Sequence 3, Appl1	1209	156.5	11.4	163	4	US-09-270-767-45162	Sequence 45162, A
1137	193.5	14.0	260	3	US-08-906-769-139	Sequence 139, App	1210	156.5	11.4	286	4	US-09-270-767-45162	Sequence 45162, A
1138	192.5	14.0	260	3	US-08-906-616-139	Sequence 139, App	1211	156	11.4	112	4	US-09-270-767-33319	Sequence 33319, A
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1140	192.5	14.0	260	3	US-09-012-431-139	Sequence 139, App	1213	154.5	11.2	204	3	US-08-906-769-147	Sequence 147, App
1141	192.5	14.0	260	3	US-09-012-692-139	Sequence 139, App	1214	154.5	11.2	204	3	US-08-906-616-147	Sequence 147, App
1142	192.5	14.0	260	3	US-08-906-613-139	Sequence 139, App	1215	154.5	11.2	204	3	US-08-639-075A-147	Sequence 147, App
1143	191	13.9	74	4	US-09-205-258-1151	Sequence 1151, App	1216	154.5	11.2	204	3	US-09-012-431-147	Sequence 147, App
1144	191	13.9	138	6	5200340-4	Patent No. 5200340	1217	154.5	11.2	204	3	US-09-012-692-147	Sequence 147, App
1145	191	13.9	138	6	5200340-4	Patent No. 5200340	1218	154.5	11.2	204	3	US-08-906-613-147	Sequence 147, App
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1148	186.5	13.6	570	4	US-10-067-442-9	Sequence 9, Appl1	1221	153.5	11.1	139	4	US-09-270-767-33665	Sequence 33665, A
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1152	182	13.2	145	3	US-08-906-616-123	Sequence 123, App	1225	149	10.8	77	3	US-09-352-616A-329	Sequence 329, App
1153	182	13.2	145	3	US-08-639-075A-123	Sequence 123, App	1226	149	10.8	77	4	US-09-232-119A-329	Sequence 329, App
1154	182	13.2	145	3	US-09-012-692-123	Sequence 123, App	1227	149	10.8	77	4	US-09-636-215-329	Sequence 329, App
1155	182	13.2	145	3	US-08-906-613-123	Sequence 123, App	1228	149	10.8	77	4	US-09-685-166A-329	Sequence 329, App
1156	181	13.2	118	4	US-09-621-976-5522	Sequence 5522, App	1229	149	10.8	77	4	US-09-688-489-329	Sequence 329, App
1157	181	13.2	133	4	US-09-949-016-7471	Sequence 7471, App	1230	149	10.8	77	4	US-09-679-426-329	Sequence 329, App
1158	180	13.1	144	3	US-09-012-431-123	Sequence 123, App	1231	149	10.8	77	4	US-09-759-143-329	Sequence 329, App
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1160	178.5	13.0	164	3	US-09-030-607-178	Sequence 178, App	1233	148.5	10.8	276	4	US-09-270-767-32048	Sequence 32048, A
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1171	178.5	13.0	164	4	US-09-651-236-178	Sequence 178, App	1244	142.5	10.4	208	3	US-08-906-616-151	Sequence 151, App
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1174	174.5	12.7	271	3	US-09-578-303-6	Sequence 6, Appl1	1247	142.5	10.4	208	3	US-09-012-692-151	Sequence 151, App
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1176	168	12.2	141	3	US-08-906-769-135	Sequence 135, App	1249	141.5	10.3	85	4	US-09-270-767-33231	Sequence 33231, A
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1178	168	12.2	141	3	US-08-639-075A-135	Sequence 135, App	1251	139	10.1	87	3	US-08-906-769-161	Sequence 161, App
1179	168	12.2	141	3	US-09-012-431-135	Sequence 135, App	1252	139	10.1	87	3	US-08-906-616-161	Sequence 161, App
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1181	168	12.2	141	3	US-08-906-613-135	Sequence 135, App	1254	139	10.1	87	3	US-09-012-431-161	Sequence 161, App
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1183	166.5	12.1	178	3	US-09-220-731-23	Sequence 23, Appl1	1256	139	10.1	87	3	US-08-906-613-161	Sequence 161, App
1184	166.5	12.1	178	4	US-09-242-999-8	Sequence 8, Appl1	1257	139	10.1	89	3	US-08-906-769-165	Sequence 165, App
1185	166	12.1	243	4	US-09-270-767-44348	Sequence 44348, A	1258	139	10.1	89	3	US-08-906-616-165	Sequence 165, App
1186	166	12.1	769	4	US-09-949-016-11019	Sequence 11019, A	1259	139	10.1	89	3	US-08-639-075A-165	Sequence 165, App
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1188	165	12.0	198	3	US-08-906-616-133	Sequence 133, App	1261	139	10.1	89	3	US-09-012-692-165	Sequence 165, App
1189	165	12.0	198	3	US-08-639-075A-133	Sequence 133, App	1262	139	10.1	89	3	US-08-906-613-165	Sequence 165, App
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1191	165	12.0	198	3	US-09-012-692-133	Sequence 133, App	1264	134	9.8	203	4	US-09-270-767-47748	Sequence 47748, A
1192	165	12.0	198	3	US-08-906-613-133	Sequence 133, App	1265	129	9.8	200	3	US-09-008-271A-5	Sequence 5, Appl1
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1194	163	11.9	190	3	US-09-206-537-4	Sequence 4, Appl1	1267	128	9.3	246	4	US-09-370-838-60	Sequence 60, Appl
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1270	126.5	9.2	160	4	US-09-270-767-48759	Sequence 48759, A	1343	117.5	8.6	396	4	US-09-800-729-86	Sequence 86, Appl
1271	126	9.2	142	3	US-08-906-769-155	Sequence 155, Appl	1344	115.5	8.4	138	4	US-09-270-767-12233	Sequence 3323, A
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1273	126	9.2	142	3	US-08-639-075A-155	Sequence 155, Appl	1346	115	8.4	80	1	US-08-485-455D-69	Sequence 69, Appl
1274	126	9.2	142	3	US-09-004-731-83	Sequence 83, Appl	1347	115	8.4	80	2	US-08-482-130C-69	Sequence 69, Appl
1275	126	9.2	142	3	US-09-012-431-155	Sequence 155, Appl	1348	115	8.4	80	2	US-08-484-211C-69	Sequence 69, Appl
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1277	126	9.2	142	3	US-09-012-692-155	Sequence 155, Appl	1350	114	8.3	330	4	US-09-270-767-47887	Sequence 47887, A
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1281	124	9.0	125	3	US-08-906-616-97	Sequence 97, Appl	1354	112	8.2	80	3	US-08-817-795-69	Sequence 69, Appl
1282	124	9.0	125	3	US-08-639-075A-97	Sequence 97, Appl	1355	112	8.2	80	3	US-08-485-443B-69	Sequence 69, Appl
1283	124	9.0	125	3	US-08-639-075A-97	Sequence 97, Appl	1356	112	8.2	80	3	US-08-639-075A-69	Sequence 69, Appl
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1285	124	9.0	125	3	US-09-012-692-97	Sequence 97, Appl	1358	112	8.2	80	3	US-09-012-692-69	Sequence 69, Appl
1286	124	9.0	125	3	US-08-906-613-97	Sequence 97, Appl	1359	112	8.2	80	3	US-08-906-613-69	Sequence 69, Appl
1287	124	9.0	125	3	PCT-US95-14442A-97	Sequence 4899, Ap	1360	112	8.2	80	5	PCT-US95-14442A-69	Sequence 69, Appl
1288	123.5	9.0	113	4	US-09-513-999C-4899	Sequence 32917, A	1361	111.5	8.1	179	4	US-09-270-767-31777	Sequence 31777, A
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1291	121.5	8.8	86	1	US-08-485-455D-53	Sequence 53, Appl	1364	110.5	8.0	99	3	US-08-906-616-93	Sequence 93, Appl
1292	121.5	8.8	86	2	US-08-482-130C-53	Sequence 53, Appl	1365	110.5	8.0	99	3	US-08-817-795-93	Sequence 93, Appl
1293	121.5	8.8	86	2	US-08-484-211C-53	Sequence 53, Appl	1366	110.5	8.0	99	3	US-08-639-075A-93	Sequence 93, Appl
1294	121.5	8.8	86	3	US-08-906-769-53	Sequence 53, Appl	1367	110.5	8.0	99	3	US-09-012-431-93	Sequence 93, Appl
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1296	121.5	8.8	86	3	US-08-817-795-53	Sequence 53, Appl	1369	110.5	8.0	99	3	US-08-906-613-93	Sequence 93, Appl
1297	121.5	8.8	86	3	US-08-485-443B-53	Sequence 53, Appl	1370	110.5	8.0	99	5	PCT-US95-14442A-93	Sequence 93, Appl
1298	121.5	8.8	86	3	US-08-639-075A-53	Sequence 53, Appl	1371	110	8.0	253	2	US-08-392-546C-2	Sequence 2, Appl
1299	121.5	8.8	86	3	US-09-012-431-53	Sequence 53, Appl	1372	109.5	8.0	33	3	US-08-944-483-27	Sequence 27, Appl
1300	121.5	8.8	86	3	US-09-012-692-53	Sequence 53, Appl	1373	107	7.8	137	4	US-09-270-767-43542	Sequence 43542, A
1301	121.5	8.8	86	3	US-08-906-613-53	Sequence 53, Appl	1374	106	7.7	157	2	US-08-811-949-41	Sequence 41, Appl
1302	121.5	8.8	86	5	PCT-US95-14442A-53	Sequence 53, Appl	1375	105.5	7.7	36	3	US-08-944-483-26	Sequence 26, Appl
1303	120.5	8.8	45	3	US-09-070-552C-4	Sequence 4, Appl1	1376	105.5	7.7	97	4	US-09-270-767-32342	Sequence 32342, A
1304	120	8.7	130	1	US-08-485-455D-67	Sequence 67, Appl	1377	105.5	7.7	97	4	US-09-270-767-47559	Sequence 47559, A
1305	120	8.7	130	2	US-08-482-130C-67	Sequence 67, Appl	1378	105.5	7.7	136	3	US-08-906-769-137	Sequence 137, Appl
1306	120	8.7	130	2	US-08-484-211C-67	Sequence 67, Appl	1379	105.5	7.7	136	3	US-08-906-616-137	Sequence 137, Appl
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1308	120	8.7	130	3	US-08-906-616-67	Sequence 67, Appl	1381	105.5	7.7	136	3	US-09-004-731-79	Sequence 79, Appl
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1310	120	8.7	130	3	US-08-485-443B-67	Sequence 67, Appl	1383	105.5	7.7	136	3	US-08-749-699-79	Sequence 79, Appl
1311	120	8.7	130	3	US-08-639-075A-67	Sequence 67, Appl	1384	105.5	7.7	136	3	US-09-012-692-137	Sequence 137, Appl
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1313	120	8.7	130	3	US-08-906-613-67	Sequence 67, Appl	1386	105.5	7.7	136	4	US-09-004-729-79	Sequence 79, Appl
1314	120	8.7	130	3	PCT-US95-14442A-67	Sequence 67, Appl	1387	102.5	7.6	441	4	US-09-949-016-10792	Sequence 79, Appl
1315	120	8.7	130	5	US-08-485-455D-63	Sequence 63, Appl	1388	102.5	7.5	80	1	US-08-485-455D-59	Sequence 59, Appl
1316	119	8.7	97	1	US-08-482-130C-63	Sequence 63, Appl	1389	102.5	7.5	80	2	US-08-482-130C-59	Sequence 59, Appl
1317	119	8.7	97	2	US-08-484-211C-63	Sequence 63, Appl	1390	102.5	7.5	80	2	US-08-484-211C-59	Sequence 59, Appl
1318	119	8.7	97	3	US-08-906-769-63	Sequence 63, Appl	1391	102.5	7.5	80	3	US-08-906-769-59	Sequence 59, Appl
1319	119	8.7	97	3	US-08-906-616-63	Sequence 63, Appl	1392	102.5	7.5	80	3	US-08-817-795-59	Sequence 59, Appl
1320	119	8.7	97	3	US-08-817-795-63	Sequence 63, Appl	1393	102.5	7.5	80	3	US-08-485-443B-59	Sequence 59, Appl
1321	119	8.7	97	3	US-08-639-075A-63	Sequence 63, Appl	1394	102.5	7.5	80	3	US-08-639-075A-59	Sequence 59, Appl
1322	119	8.7	97	3	US-09-012-431-63	Sequence 63, Appl	1395	102.5	7.5	80	3	US-09-012-431-59	Sequence 59, Appl
1323	119	8.7	97	3	US-08-906-613-63	Sequence 63, Appl	1396	102.5	7.5	80	3	US-09-012-692-59	Sequence 59, Appl
1324	119	8.7	97	3	US-08-906-613-63	Sequence 63, Appl	1397	102.5	7.5	80	3	US-08-906-613-59	Sequence 59, Appl
1325	119	8.7	97	3	US-08-906-613-63	Sequence 63, Appl	1398	102.5	7.5	80	5	PCT-US95-14442A-59	Sequence 59, Appl
1326	119	8.7	97	5	PCT-US95-14442A-63	Sequence 63, Appl	1400	101.5	7.4	117	4	US-09-270-767-33317	Sequence 33317, A
1327	119	8.7	97	5	US-08-906-769-157	Sequence 157, Appl	1401	101.5	7.4	117	4	US-09-270-767-47534	Sequence 47534, A
1328	118	8.6	130	3	US-08-906-616-157	Sequence 157, Appl	1402	101	7.4	125	4	US-09-270-767-33002	Sequence 33002, A
1329	118	8.6	130	3	US-08-639-075A-157	Sequence 157, Appl	1403	101	7.4	125	4	US-09-270-767-48219	Sequence 48219, A
1330	118	8.6	130	3	US-09-012-431-157	Sequence 157, Appl	1404	101	7.4	339	4	US-09-543-681A-9665	Sequence 6865, Ap
1331	118	8.6	130	3	US-08-906-613-157	Sequence 157, Appl	1405	100.5	7.3	55	4	US-08-842-076D-22	Sequence 22, Appl
1332	118	8.6	130	3	US-08-906-769-153	Sequence 153, Appl	1406	100	7.3	68	1	US-08-485-455D-77	Sequence 77, Appl
1333	117.5	8.6	144	3	US-08-906-616-153	Sequence 153, Appl	1407	100	7.3	68	2	US-08-482-130C-77	Sequence 77, Appl
1334	117.5	8.6	144	3	US-08-639-075A-153	Sequence 153, Appl	1408	100	7.3	68	2	US-08-484-211C-77	Sequence 77, Appl
1335	117.5	8.6	144	3	US-09-004-731-81	Sequence 81, Appl	1409	100	7.3	68	3	US-08-906-769-77	Sequence 77, Appl
1336	117.5	8.6	144	3	US-09-012-431-81	Sequence 81, Appl	1410	100	7.3	68	3	US-08-817-795-77	Sequence 77, Appl
1337	117.5	8.6	144	3	US-08-749-699-81	Sequence 81, Appl	1411	100	7.3	68	3	US-08-485-443B-77	Sequence 77, Appl
1338	117.5	8.6	144	3	US-09-012-692-153	Sequence 153, Appl	1412	100	7.3	68	3	US-08-639-075A-77	Sequence 77, Appl
1339	117.5	8.6	144	3	US-08-906-613-153	Sequence 153, Appl	1413	100	7.3	68	3	US-09-012-431-77	Sequence 77, Appl
1340	117.5	8.6	144	3	US-08-906-613-153	Sequence 153, Appl	1414	100	7.3	68	3		

Query	Db	Sequence	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
1	MGISTILLICVGLGSAATPKIFNGTEGCRNQPOMVGLFESTSLRCGGVLLIDHRWTLTA	60	98.9%	1359.5	249	249	0	0	1	1
2	3	MGISTILLICVGLGSAATPKIFNGTEGCRNQPOMVGLFESTSLRCGGVLLIDHRWTLTA	62	98.9%	1359.5	249	0	0	1	1
3	61	AHCGSRWYWRIGEHSLQDLMTQDRIHSGFVTPHRYGASTSHENHLLRLRLPLRV	120	98.9%	1359.5	249	0	0	1	1
4	63	AHCGSRWYWRIGEHSLQDLMTQDRIHSGFVTPHRYGASTSHENHLLRLRLPLRV	121	98.9%	1359.5	249	0	0	1	1
5	121	TSSVQPLPLPNDCAITAGTECHVSGMGITNHPNPPDLLQCLNLSIVSHATCHEVYPERI	180	98.9%	1359.5	249	0	0	1	1
6	122	TSSVQPLPLPNDCAITAGTECHVSGMGITNHPNPPDLLQCLNLSIVSHATCHEVYPERI	181	98.9%	1359.5	249	0	0	1	1
7	181	TSMNVCAAGVPGQDACQSGSGRPVLCGGVLLQSLVSMGSGVPGGQGIQGVYTIICKYDWM	240	98.9%	1359.5	249	0	0	1	1
8	182	TSMNVCAAGVPGQDACQSGSGRPVLCGGVLLQSLVSMGSGVPGGQGIQGVYTIICKYDWM	241	98.9%	1359.5	249	0	0	1	1
9	241	IRIMIMNN 248	248	98.9%	1359.5	249	0	0	1	1
10	242	IRIMIMNN 249	249	98.9%	1359.5	249	0	0	1	1

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6948
LENGTH: 254
TYPE: PRT
ORGANISM: Human
US-09-949-016-6948

Query Match 94.7%; Score 1301; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.5e-118;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLIFLLCVLGISQATPKIFNGTECGRNSOPWVGLFEGTSLRCGGVLIIDHRWVLTAA 60
DB 1 MGSLIFLLCVLGISQATPKIFNGTECGRNSOPWVGLFEGTSLRCGGVLIIDHRWVLTAA 60
QY 61 AHGSGRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
DB 61 AHGSGRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
QY 121 TSSVQPLPLPNDCAATAGTECHVSGWGITNHRNPPDLLQCLNLSIVSHATCHGVYGR 180
DB 121 TSSVQPLPLPNDCAATAGTECHVSGWGITNHRNPPDLLQCLNLSIVSHATCHGVYGR 180
QY 181 TSNMVCAGVPGDACCQDSGGPLVCGGVLQGLVSWGSGVPCGQDGPVYTYIC 235
DB 181 TSNMVCAGVPGDACCQDSGGPLVCGGVLQGLVSWGSGVPCGQDGPVYTYIC 235

RESULT 3

US-09-244-111-6
Sequence 6, Application US/09244111
Patent No. 6566498

GENERAL INFORMATION:

APPLICANT: Ni, et al.

TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides

FILE REFERENCE: P391

CURRENT APPLICATION NUMBER: US/09/244,111

CURRENT FILING DATE: 1999-02-04

EARLIER APPLICATION NUMBER: 60/073,961

EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 6

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-09-244-111-6

Query Match 59.0%; Score 811; DB 4; Length 162;
Best Local Similarity 64.1%; Pred. No. 3.8e-71;

Matches 159; Conservative 0; Mismatches 3; Indels 86; Gaps 3;

QY 1 MGSLIFLLCVLGISQATPKIFNGTECGRNSOPWVGLFEGTSLRCGGVLIIDHRWVLTAA 60
DB 1 MGSLIFLLCVLGISQATPKIFNGTECGRNSOPWVGLFEGTSLRCGGVLIIDHRWVLTAA 60
QY 61 AHGSGRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
DB 61 AHGSGRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120

QY 121 TSSVQPLPLPNDCAATAGTECHVSGWGITNHRNPPDLLQCLNLSIVSHATCHGVYGR 180
DB 70 -----PDLQCLNLSIVSHATCHGVYGR 94
QY 181 TSNMVCAGVPGDACCQDSGGPLVCGGVLQGLVSWGSGVPCGQDGPVYTYICRYV 240
DB 95 TSNMVCAGVPGDACCQDSGGPLVCGGVLQGLVSWGSGVPCGQDGPVYTYICRYV 240
QY 241 IRMIMRN 248
DB 155 IRMIMRN 162

RESULT 4

US-09-618-259-7
Sequence 7, Application US/09618259
Patent No. 6642013

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease

FILE REFERENCE: D6020CIP2

CURRENT APPLICATION NUMBER: US/09/618,259

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: US 09/127,444

PRIOR FILING DATE: 1998-08-21

NUMBER OF SEQ ID NOS: 72

SEQ ID NO 7

LENGTH: 260

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Amino acid sequence of TADG-14 protein

US-09-618-259-7

Query Match 45.9%; Score 630.5; DB 4; Length 260;
Best Local Similarity 50.2%; Pred. No. 2.5e-53;
Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;

QY 5 IRLI---CVLGISQATPKIFNGTECGRNSOPWVGLFEGTSLRCGGVLIIDHRWVLTAA 61
DB 13 MFLLLGAMWAGHSRAQEDKVLGHCQPHSQPWOALFOGQOLCGVVGNNVLTAA 72
QY 62 HCSGRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGAST-SHEHDLRLRLPVRV 120
DB 73 HCKKPYTYRLGHSIQNDPQEGELPVQSIHPCYNSDVEDHNDLMLQRLQDASL 132
QY 121 TSSVQPLPLPNDCAATAGTECHVSGWGITNHRNPPDLLQCLNLSIVSHATCHGVYGR 180
DB 133 GSKVKPISLADHCTQPGKCTVSGWGTVPENPFDTLNCAEVKIFPOKCEDAVPGQI 192
QY 181 TSNMVCAGVPGDACCQDSGGPLVCGGVLQGLVSWGSGVPCGQDGPVYTYICRYV 240
DB 193 TDGMVACGSSKADTQDSGGPLVCGDGLQGITWSG-DPCGRSDKPVYTYICRYLDM 251
QY 241 IRMIM 245
DB 252 IKKII 256

RESULT 5

US-09-070-526-2

Sequence 2, Application US/09070526
Patent No. 6100059

GENERAL INFORMATION:

APPLICANT: SOUTHAN, CHRISTOPHER

APPLICANT: CLINKENBEARD, HELEN

APPLICANT: BURGESS, NICOLA

TITLE OF INVENTION: No. 6100059el Compounds

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAINER & PRESTIA

STREET: P.O. BOX 980

```
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070.526
FILING DATE: 30-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9711952.3
FILING DATE: 9-JUN-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-070-526-2
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Query Match 45.6%; Score 626.5; DB 3; Length 260;
Best Local Similarity 50.4%; Pred. No. 6.2e-53;
Matches 122; Conservative 23; Mismatches 92; Indels 5; Gaps 3;
```

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QY 5 IPLL--CVIGLSQATPKIFNGTECGRNSQPMQVGLFBGTSIRCGGVLTIDHRWVLTAA 61
D 13 MFLLLGGAMAGHRAQEDKVLGHECCQPHSQPMQALFQGRQLLCGGVLVGMWVLTAA 72
QY 62 HCGSSRYWVRLGHSLSQLDWTQIRHSGFSVTHPGYLGAST-SHEHDLRLRLRLPRV 120
D 73 HCKKPKTVRLGDSHLQKQPEDEIPVQSIPIPCYNSSVEDHNDMLQLRDAQSL 132
QY 121 TSSVQPLPLPNDCACTAGTECHVSGMGITNHPNPFDDLLQCLNLSIVSHATCHGVPGRI 180
D 133 GSKVKPISLADHCTQPGQKCTVSGMGVTSFRENFPDTLNCABYKIFPQKKCEADYFGQI 192
QY 181 TSNMVCAGVPGDACCQDGGPILVCGVLTGLVSWGSGVPGCGDGIPIGVYTYIKCYVDW 240
D 193 TDGWCAGSSKGAADTCQDGGGPIVCDGALQGITSMGS-DPCGRSDKRGVYTNICRYLDW 251
QY 241 IR 242
D 252 IK 253
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RESULT 6
US-09-025-059-3
Sequence 3, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
```

```
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025.059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1020091
US-09-025-059-3
```

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Query Match 45.3%; Score 622.5; DB 3; Length 260;
Best Local Similarity 49.0%; Pred. No. 1.5e-52;
Matches 121; Conservative 29; Mismatches 93; Indels 5; Gaps 3;
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QY 5 IPLLCV--LGISQATPKIFNGTECGRNSQPMQVGLFBGTSIRCGGVLTIDHRWVLTAA 61
D 13 ILLLLFMGAMAGLTRAQGSKILLEGRECIPIHSQPMQALFQGERLICGGVLVGDHRWVLTAA 72
QY 62 HCGSSRYWVRLGHSLSQLDWTQIRHSGFSVTHPGYLGAS-TSEHDLRLRLRLPRV 120
D 73 HCKKQKYSVRLGDSLSQSRDQPEDEIQVAQSIQHPCTNNSNPEDHSHDMLIRLQNSANL 132
QY 121 TSSVQPLPLPNDCACTAGTECHVSGMGITNHPNPFDDLLQCLNLSIVSHATCHGVPGRI 180
D 133 GDKVKPVLQNLCPKVGQKCLISGMGTVTSFQENFPMTLNCABYKIVSQNKCEADYFGQI 192
QY 181 TSNMVCAGVPGDACCQDGGPILVCGVLTGLVSWGSGVPGCGDGIPIGVYTYIKCYVDW 240
D 193 TEGWVCAGSSNGADTCQDGGGPIVCDGMLQGITSMGS-DPCGRPEKRGVYTNICRYTDW 251
QY 241 IRMTNR 247
D 252 IKKTMN 258
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RESULT 7
US-09-008-271A-7
Sequence 7, Application US/09008271A
Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Tang, Tom Y.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
```

1 NUMBER OF SEQUENCES: 24
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Incyte Pharmaceuticals, Inc.
4 STREET: 3174 Porter Dr.
5 CITY: Palo Alto
6 STATE: CA
7 COUNTRY: USA
8 ZIP: 94304
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Diskette
12 COMPUTER: IBM Compatible
13 OPERATING SYSTEM: DOS
14 SOFTWARE: FastSeq for Windows Version 2.0
15
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/008,271A
18 FILING DATE: 16-Jan-1998
19
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: <Unknown>
22 FILING DATE: <Unknown>
23
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Mohan-Peterson, Sheila
26 REGISTRATION NUMBER: 41,201
27 REFERENCE/DOCKET NUMBER: PF-0458 US
28
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 650-855-0555
31 TELEFAX: 650-845-4166
32
33 INFORMATION FOR SEQ ID NO: 7:
34
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 260 amino acids
37 TYPE: amino acid
38 STRANDEDNESS: single
39 TOPOLOGY: linear
40
41 IMMEDIATE SOURCE:
42 LIBRARY: COLNOT27
43 CLONE: 1798496
44
45 SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
46
47 US-09-008-271A-7

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RESULT 8
US-09-618-259-8
; Sequence 8, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020C1P2
; CURRENT APPLICATION NUMBER: US/09/618,259

```

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; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 8
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of mouse neuropsin homologous
; OTHER INFORMATION: to TAD5-14; accession no. D30785
US-09-618-259-8

```

Query Match	45.3%	Score 622.5	DB 4	Length 260
Best local Similarity	49.0%	Pred. No. 1.5e-52		
Matches 121	Conservative 28	Mismatches 93	Indels 5	Gaps 3
Qy	5	ITLLICV--IGLSGATPKIENGTEGCRNSQPMVQGLFEGSTLRGCVYLIDHRWLTAA	61	
Db	13	ITLLIFMGAMGLTTPAQSGLTEGRECI PHSQPMQAAIFGGERLIGCVYLVEDRWLTAA	72	
Qy	62	HCSGRYRWYRAGEISLSGLDWTBQIRHSGRSYVHPVLAAS-TSHHDRLRLRLPLRV	120	
Db	73	HCKKQKTSYRLGDHSLGSRDQPEDEIYVAOSTIHPCCINNSNPEDSHDMLIRLONSANL	132	
Qy	121	TSSVQPLRPNDCAITAGTECHVSGMGITTHPRNPPDLLQCLNLSIVSHATCHGVYPGRI	180	
Db	133	GDKVPEVLTALICRPVQOKCISISGWTGTVTSPQENFPNTLNCABVKYSQNKCEBAYPGKI	192	
Qy	181	TSSNWTCAGGVGDACGCGSGGPIYVCGVYQGLVMSGISVPGCGOGIGVYTYIKCYDWM	240	
Db	193	TBGMVCAASSNGADLTCCQDSDGGPVLCDGMIGITTSWGS-DPCGKEKPGVYTKICRYTTW	251	
Qy	241	IRIMIMEN	247	
Db	252	IKKTMDN	258	

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RESULT 9
US-09-205-258-427
/ Sequence 427, Application US/09205258
/ Patent No. 6525174
/ GENERAL INFORMATION:
/ APPLICANT: Young et al.
/ TITLE OF INVENTION: 207 Human Secreted Proteins
/ FILE REFERENCE: P2007P1
/ CURRENT APPLICATION NUMBER: US/09/205,258
/ CURRENT FILING DATE: 1998-12-04
/ EARLIER APPLICATION NUMBER: PCT/US98/11422
/ EARLIER FILING DATE: 1998-06-04
/ EARLIER APPLICATION NUMBER: 60/048,885
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,375
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,881
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,880
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,896
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,020
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,876
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,895
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,884
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,894
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,971
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,964

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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070, 923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092, 921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094, 657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 427
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-427

Query Match 45.0%; Score 618.5; DB 4; Length 250;
Best Local Similarity 48.2%; Pred. No. 3.5e-52;
Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;

QY 3 LSTLLLCVGLGSAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLDHRVNLTAH 62
DB 4 LQILLALATGLVGGET-RIIKGFECCKPHSQPMQVGLFEGTSLRCGGVLDHRVNLTAH 62
QY 63 CSGRYVVRIGEHSLQSDWTEQIRHSGFVTHPGVLA--STSHEDLRLLRLPVRV 120

DB 63 CLKPRYIVHLGQHNLOKEEGCEQTRTATESPPHGFNNLSLPNKDRHIDMLVKMASPVSI 122
QY 121 TSSVQPLPLPNDCTAGTECHVSGWGITNHPRNPFPDLOCLNLSYSHATCHVPGRI 180
DB 123 TWAVRPLTSSRCTAGTSCILISGSGTSSPQLRPLPTRLRCANTTIEHQRCENAYPGNI 182
QY 181 TSNMVACG-GVPGODACQDPSGGGLVCGGVLDGLVSGSVGPCGQDGIPIGYTYICKVVD 239
DB 183 TDTWVCASVQEGKDSQSGDSGGLVVCNOSLQGIISMGQ-DPCAITRKPGVYTKVCKYVD 241
QY 240 WIRMIMENN 248
DB 242 WIDETMKN 250

RESULT 10
US-09-025-059-1
Sequence 1, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGUT110
CLONE: 2723646
US-09-025-059-1

Query Match 45.0%; Score 618.5; DB 3; Length 282;
Best Local Similarity 48.2%; Pred. No. 4.1e-52;
Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;

QY 3 LSTLLLCVGLGSAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLDHRVNLTAH 62
DB 36 LQILLALATGLVGGET-RIIKGFECCKPHSQPMQVGLFEGTSLRCGGVLDHRVNLTAH 94
QY 63 CSGRYVVRIGEHSLQSDWTEQIRHSGFVTHPGVLA--STSHEDLRLLRLPVRV 120

Db 95 CLKRYIVHLGQHNLOKEBCEQTRTATESFPHFGFNLSLPNKDHRNDIMLVMAASVSI 154
QY 121 TSSVOPPLPNDATAGTEGVSGMGITNHRNPFDDLOCLNLSTVSHATCHGVYPRGI 180
Db 155 TMAVRPLTSSRCVTACTSCLISGWSSTSPQURLPHTLRKANITITIEHOKENAYPGNI 214
QY 181 TSNMVCAG-GVPGQDACCQDSSGGLVCGVYLQGLVSGSVPCGQDGIPIGVYTIKCYVD 239
Db 215 TDTMVCASVQEGGKDCSQDSSGGLVCGVYVONQSLGIIISMGQ-DPCAIRKRGVYTKVCKYVD 273
QY 240 WIMIMRNN 248
Db 274 WIOETMKNN 282

RESULT 11
US-09-386-642-13
Sequence 13, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jensen
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 288
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
US-09-386-642-13
Query Match 43.9%; Score 602.5; DB 4; Length 288;
Best Local Similarity 51.1%; Pred. No. 1.5e-50;
Matches 116; Conservative 21; Mismatches 87; Indels 3; Gaps 3;

QY 21 KIFNTEC-GRNSOPWVGFEGTSLRCGVLIDHRVLTAAHSGSRVYRLGHSLSQ 79
Db 51 KIVGYNCLERHSGPWQALFQGOQLCGVVGWNLTAHCKKPYTYRLDHSILON 110
QY 80 LDWTEQIRHSGFSVYHPGYLGAFT-SHHDLRLRLPVRVTSVOPPLPNDCATAGT 138
Db 111 KDGPQELIPVQSIHPFCYNSDVEDNHDMLQDLQDAGLSKVKFISLADHCTQPGQ 170
QY 139 ECHVSGMGITNHRNPFDDLOCLNLSTVSHATCHGVYPRGITSNMVCAGVPGQDACCQ 198
Db 171 KCTVSGMGITVTSFPENFPDITNCAEVKIFPQKCEDAVPGQITDGMVCAGSSKADTCQG 230
QY 199 DSGGPLVCGVYLQGLVSGSVPCGQDGIPIGVYTIKCYVDIMRNN 245
Db 231 DSGGPLVCGVYLQGLVSGSVPCGQDGIPIGVYTIKCYVDIMRNN 276

RESULT 12
US-09-386-642-14
Sequence 14, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jensen
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 14
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-14

Query Match 43.6%; Score 598.5; DB 4; Length 289;
Best Local Similarity 49.1%; Pred. No. 3.8e-50;
Matches 114; Conservative 34; Mismatches 79; Indels 5; Gaps 4;
QY 21 KIFNTEC-GRNSOPWVGFEGTSLRCGVLIDHRVLTAAHSGSRVYRLGHSLSQ 79
Db 51 KIVGYNCLERHSGPWQALFQGOQLCGVVGWNLTAHCKKPYTYRLDHSILON 110
QY 80 LDWTEQIRHSGFSVYHPGYLGAFT-SHHDLRLRLPVRVTSVOPPLPNDCATAG 137
Db 111 ECGEQTRTATESFPHFGFNLSLPNKDHRNDIMLVMAASVSIWAVRPLTSSRCVTAG 170
QY 138 TECHVSGMGITNHRNPFDDLOCLNLSTVSHATCHGVYPRGITSNMVCAG-GVPGQDACC 196
Db 171 TSCLSGWSSTSPQURLPHTLRKANITITIEHOKENAYPGNITDTMVCASVQEGKDC 230
QY 197 QGDSGGLVCGVYLQGLVSGSVPCGQDGIPIGVYTIKCYVDIMRNN 248
Db 231 QGDSGGLVCGVYLQGLVSGSVPCGQDGIPIGVYTIKCYVDIMRNN 281

RESULT 13
US-08-944-483-24
Sequence 24, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLLITS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183, US. 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623

TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-24

Query Match 43.5%; Score 597.5; DB 3; Length 248;
Best Local Similarity 47.8%; Pred. No. 3.9e-50;
Matches 119; Conservative 36; Mismatches 87; Indels 7; Gaps 6;

QY 3 LSLILLCVGLSGAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLLDHRVLTAAH 62
DB 4 LQLLALATGLVGERT-RITKGFEC-PHSQPMQALFK-TRLLCGATLLPFRMLTAAH 60
QY 63 CSGSRVWVRLGEHSLQDLMTQEIIRHSGSVTHPGYLGA--STSHEHDLRLRLPVRV 120
DB 61 CLKRRTYVHLGQNLQKEEGCEQRTATSEFPHPGPNNSLPKXDRNDIMLVKMAAPVSI 120
QY 121 TSSVQPLPLPNDCAATAGTECHVSGMGITNHPNPFDLLQCLNLISVSHATCHGVYPR 180
DB 121 TWAVRPLTISRCTAGTSCGISGWSSTSPQLRLPHTLRCAINITIIEHQKCNAYPGNI 180
QY 181 TSNMVCAG-GVPGQDACCGDSGGLVCGGVLOGLVSMGVSVPCCGDDGIPGVYTYICKYVD 239
DB 181 TDIVWCASVQEGKDCGDSGGLVCGVLOGIISWQ-DPCAITRRKPGVYTRVCKYVD 239
QY 240 WIRMIRNN 248
DB 240 WIGETMKN 248

RESULT 14
US-08-956-267A-2
Sequence 2, Application US/08956267A
Patent No. 5945328
GENERAL INFORMATION:
APPLICANT: WOLDIKE, Helle Fabricius
APPLICANT: KJELDSEN, Thomas Borjlum
TITLE OF INVENTION: A Process For Producing Trypsin
TITLE OF INVENTION: (Trypsinogen)
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 59453280 No. 5945328disk of No. 59453280th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,267A
FILING DATE: 22-OCT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4500,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-956-267A-2

Query Match 41.7%; Score 573; DB 2; Length 247;
Best Local Similarity 45.6%; Pred. No. 9.3e-46;
Matches 113; Conservative 42; Mismatches 83; Indels 10; Gaps 5;

QY 6 FLILLCVGLSGAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLLDHRVLTAAH 61
DB 5 FVLALIGAANAFTDDDDKIVGGYTCAANSIPYQVSLNSGSHF-CGGSILNSQMVVSA 63
QY 62 HCSGRVWVRLGEHSLQDLMTQEIIRHSGSVTHPGYLGA--STSHEHDLRLRLPVRV 121
DB 64 HCYSRIQVRLGEBNIDVLEGNQFIVAKIITHPNFG--NTLDNDIMLIKSSPATLN 121
QY 122 SSVQPLPLPNDCAATAGTECHVSGMGITNHPNPFDLLQCLNLISVSHATCHGVYPR 181
DB 122 SRVATVSLPRSCAAAGTECLISGWNKTSKSSYPSLLQCLKAPVLDSSCKSSYPQIT 181
QY 182 SNMVCAGVPGQDACCGDSGGLVCGGVLOGLVSMGVSVPCCGDDGIPGVYTYICKYVD 240
DB 182 GNMICVGFLEGGKDCGDSGGLVCGVLOGIISWQ--GCAQKPKPGVYTRVCKYVD 239
QY 241 IRMIRNN 248
DB 240 IQOTIAAN 247

RESULT 15
US-09-949-016-8166
Sequence 8166, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 8166
LENGTH: 290
TYPE: PRT
ORGANISM: Human
US-09-949-016-8166

Query Match 41.3%; Score 567; DB 4; Length 290;
Best Local Similarity 46.8%; Pred. No. 4.4e-47;
Matches 116; Conservative 36; Mismatches 80; Indels 16; Gaps 6;

QY 13 GLSGAATPKIFN-----GTECGRNSQPMQVGLFEGTSLRCGGVLLDHRVLTAAH 62
DB 31 GVSQESS-KVLTNTGTSGLPGGYTCFPHSQPMQALLVQGRLLCGGVLVHPKVVLTAAH 89
QY 63 CSGSRVWVRLGEHSLQDLMTQEIIRHSGSVTHPGYLGA--STSHEHDLRLRLPVRV 120
DB 90 CLKELKRVYLGKHALGVEAGEOVRVYHSTPHPEYRSPFHLNHDHIMLBLSQSPVL 149
QY 121 TSSVQPLPLP-NDCAATAGTECHVSGMGITNHPNPFDLLQCLNLISVSHATCHGVYPR 179
DB 150 TGYIQTLPFHNHRLTGTTCRVSQWGTTSPPQNVYKTIQCANIQLRSDECHQVYPRG 209
QY 180 ITSNMVCAGVPGQDACCGDSGGLVCGGVLOGLVSMGVSVPCCGDDGIPGVYTYICKYVD 238
DB 210 ITDMLCAGTKEGGKDCGDSGGLVCGVLOGIISWQDF-PCGQDPRPGVYTRVCKYVD 268

Qy	239	DWIRMR	246
			:
Db	269	LWIRRTIR	276

Search completed: March 5, 2005, 18:16:40
Job time : 46 secs

GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: March 5, 2005, 18:13:34 ; Search time 166 Seconds
(without alignments)
577.811 Million cell updates/sec

Title: US-10-006-116A-194
Sequence: 1374
Perfect score: 1 MGSIFLLCTVGLSQATP.....GVYTYICKYVIMIMKNN 248
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 segs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: Genesegp1980s:*
2: Genesegp1990s:*
3: Genesegp2000s:*
4: Genesegp2001s:*
5: Genesegp2002s:*
6: Genesegp2003as:*
7: Genesegp2003bs:*
8: Genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AA821304	standard;	protein;	248 AA.		
DE	Human KLU-L5	protein #4.				
PN	WO200053776-A2.					
PD	14-SEP-2000.					
PA	(MOUN) MOUNT SINAI HOSPITAL.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 2						
ID	AA824428	standard;	protein;	248 AA.		
DE	Human PRO1303	protein sequence SEQ ID NO:203.				
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 3						
ID	AA824032	standard;	protein;	248 AA.		
DE	Human PRO1303	protein sequence SEQ ID NO:33.				
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 4						
ID	AA193933	standard;	protein;	248 AA.		
DE	Human PRO1303	(UNQ669) amino acid sequence SEQ ID NO:194.				
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 5						
ID	AA423994	standard;	protein;	248 AA.		
DE	Human EST encoded	protein SEQ ID NO: 1519.				
PN	WO200154477-A2.					
PD	02-AUG-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match	100.0%;	Score 1374;	DB 4;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 6						
ID	AA86142	standard;	protein;	248 AA.		

DE	Protein of the invention #54.					
PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 4;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 7						
ID	ABO33635	standard;	protein;	248 AA.		
DE	Novel human secreted and transmembrane protein PRO1303.					
PN	US2003073130-A1.					
PD	17-APR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 6;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 8						
ID	ABO44488	standard;	protein;	248 AA.		
DE	Human secreted/transmembrane protein PRO1303.					
PN	US2003044841-A1.					
PD	06-MAR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 7;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 9						
ID	ABO33512	standard;	protein;	248 AA.		
DE	Novel human secreted and transmembrane protein PRO1303.					
PN	US2003073129-A1.					
PD	17-APR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 7;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 10						
ID	ADCI8063	standard;	protein;	248 AA.		
DE	Human PRO polypeptide #54.					
PN	US2003064925-A1.					
PD	03-APR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 7;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 11						
ID	ADD70709	standard;	protein;	248 AA.		
DE	Human secreted/transmembrane protein PRO1303.					
PN	US2003096625-A1.					
PD	29-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 7;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 12						
ID	ADD39786	standard;	protein;	248 AA.		
DE	Human secreted/transmembrane protein PRO1303.					
PN	US2003083462-A1.					
PD	01-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 7;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 13						
ID	ADD70232	standard;	protein;	248 AA.		
DE	Human secreted/transmembrane protein PRO1303.					
PN	US2003054406-A1.					
PD	20-MAR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 7;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 14						
ID	ADD38353	standard;	protein;	248 AA.		
DE	Human secreted/transmembrane protein PRO1303.					
PN	US2003096955-A1.					
PD	22-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 7;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 15						
ID	ADD39309	standard;	protein;	248 AA.		
DE	Human secreted/transmembrane protein PRO1303.					

PN US2003096954-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 16
 ID ADD38832 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003092061-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 17
 ID ADD40263 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003082627-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 18
 ID ADE50484 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 19
 ID ADE20096 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 20
 ID ADE50007 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 21
 ID ADE21565 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003082628-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 22
 ID ADF29990 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 23
 ID ADF55883 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 24
 ID ADH99387 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003065142-A1.
 PD

PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 25
 ID ADE96567 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 8; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 26
 ID ADF25878 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 8; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 27
 ID ADF24777 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003198993-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 8; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 28
 ID ADF29513 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003203401-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 8; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 29
 ID ADE97044 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003195334-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 8; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 30
 ID ADH03082 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003216562-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 8; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 31
 ID ADH04036 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003220471-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 8; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 32
 ID ADH03559 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2003224478-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1374; DB 8; Length 248;
 Best Local Similarity 100.0%; Pred. No. 5e-98;
 RESULT 33
 ID ADH04513 standard; protein; 248 AA.
 DE Human secreted/transmembrane protein PRO1303.
 PN US2004005626-A1.
 PD 08-JAN-2004.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 34
ID ADH61514 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 35
ID ADN10927 standard; protein; 248 AA.
DE Human kallikrein 12, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 36
ID ADJ94713 standard; protein; 248 AA.
DE Human secreted/transmembrane protein PRO1303.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 37
ID ADT94373 standard; protein; 248 AA.
DE Human PRO1303 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 38
ID AAO29516 standard; protein; 248 AA.
DE Human kallikrein-like protein 5 (18817).
PN WO2003039475-A2.
PD 15-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.5%; Score 1367; DB 6; Length 248;
Best Local Similarity 99.6%; Pred. No. 1.7e-97;
RESULT 39
ID AAB21303 standard; protein; 254 AA.
DE Human KLK-L5 protein #3.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 94.7%; Score 1301; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.2e-92;
RESULT 40
ID ABG66676 standard; protein; 254 AA.
DE Human novel polypeptide #11.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 94.7%; Score 1301; DB 5; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.2e-92;
RESULT 41
ID ADN10926 standard; protein; 254 AA.
DE Human kallikrein 12, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 94.7%; Score 1301; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.2e-92;
RESULT 42
ID ADP6174 standard; protein; 254 AA.
DE Human PRO protein sequence SEQ ID NO:2150.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match 94.7%; Score 1301; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.2e-92;
RESULT 43
ID AAB21301 standard; protein; 184 AA.
DE Human KLK-L5 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 74.2%; Score 1019; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.5e-71;
RESULT 44
ID AAY28642 standard; protein; 162 AA.
DE Human secreted protein from cDNA clone HKAFF61.
PN WO9940183-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 59.0%; Score 811; DB 2; Length 162;
Best Local Similarity 64.1%; Pred. No. 8.1e-55;
RESULT 45
ID AAY2852 standard; protein; 260 AA.
DE Human serine protease protein sequence.
PN JP1125765-A.
PD 24-AUG-1999.
PA (SUNR) SUNTORY LTD.
Query Match 45.9%; Score 630.5; DB 2; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 46
ID AAY41744 standard; protein; 260 AA.
DE Human PRO322 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 2; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 47
ID AAY03220 standard; protein; 260 AA.
DE Amino acid sequence of human tumour antigen derived gene-14 protein.
PN WO9809138-A1.
PD 25-FEB-1999.
PA (UVAR-) UNITV ARKANSAS.
Query Match 45.9%; Score 630.5; DB 2; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 48
ID AAB21322 standard; protein; 260 AA.
DE Human neuropsin.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.9%; Score 630.5; DB 3; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 49
ID AAB44300 standard; protein; 260 AA.
DE Human PRO322 (UNQ283) protein sequence SEQ ID NO:395.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 3; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 50
ID AAY51131 standard; protein; 260 AA.
DE Human neuropsin protein.
PN JP1318461-A.
PD 24-NOV-1999.
PA (SHIO/) SHIOZAKA S.
Query Match 45.9%; Score 630.5; DB 3; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 51
ID AAU12369 standard; protein; 260 AA.
DE Human PRO322 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 45.9%; Score 630.5; DB 4; Length 260;
PRED. NO. 1.1e-40;
RESULT 52
ID AAB53087 standard; protein; 260 AA.
DE Human angiogenesis-associated protein PRO322, SEQ ID NO:127.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 4; Length 260;
PRED. NO. 1.1e-40;
RESULT 53
ID ABG23373 standard; protein; 260 AA.
DE Novel human diagnostic protein #3364.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 4; Length 260;
PRED. NO. 1.1e-40;
RESULT 54
ID ABB84852 standard; protein; 260 AA.
DE Human PRO322 protein sequence SEQ ID NO:72.
PN WO20020690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 5; Length 260;
PRED. NO. 1.1e-40;
RESULT 55
ID AAU81959 standard; protein; 260 AA.
DE Human PRO322.
PN WO200109327-A2.
PD 08-FEB-2001.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 5; Length 260;
PRED. NO. 1.1e-40;
RESULT 56
ID ABB95458 standard; protein; 260 AA.
DE Human angiogenesis related protein PRO322 SEQ ID NO: 72.
PN WO200206284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
DE Human PRO322.
PN WO200206284-A2.
PD 31-JAN-2002.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERB/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODD/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANT/) PAN J.
PA (PAON/) PRONTI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 5; Length 260;
PRED. NO. 1.1e-40;
RESULT 57
ID ADI17076 standard; protein; 260 AA.
DE Human NOVX protein homologue SegID 612.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 5; Length 260;
PRED. NO. 1.1e-40;
RESULT 58
ID ABO17813 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 59
ID ABO25246 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 60
ID ABU81067 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 61
ID ABU72252 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 62
ID ADA05702 standard; protein; 260 AA.
DE Human NOV11h protein SEQ ID NO:62.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 63
ID ABU6767 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 64
ID ABU84932 standard; protein; 260 AA.
DE Human secreted and transmembrane PRO polypeptide #8.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 65
ID ABUS9848 standard; protein; 260 AA.
DE Novel secreted and transmembrane protein PRO322.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 66
ID ABU61130 standard; protein; 260 AA.
DE Human PRO322 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 67
ID ABO25038 standard; protein; 260 AA.
DE Human secreted/transmembrane protein (PRO) #198.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 45.9%; Score 630.5; DB 6; Length 260;
PRED. NO. 1.1e-40;
RESULT 68
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ID ABU80399 standard; protein; 260 AA.
DE Human secreted/transmembrane protein PRO322.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 69
ID ABU67043 standard; protein; 260 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 396.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 70
ID ADA45915 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 71
ID ADA76346 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 72
ID ADA18996 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 73
ID ADA61619 standard; protein; 260 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 74
ID ADA19404 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 75
ID ADB27945 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 76
ID ADA86424 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 77
ID ADB15986 standard; protein; 260 AA.

DE Human PRO polypeptide #198.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 78
ID ADA47774 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 79
ID ADA67569 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 80
ID ADB30576 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 81
ID ADA85872 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 82
ID ADA97084 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 83
ID ADA79388 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 84
ID ADA87527 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 85
ID ADB16729 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 86
ID ADA91821 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.

PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 87
ID ADB14884 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 88
ID ADA24934 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 89
ID ADB18845 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 90
ID ADA94060 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 91
ID ADB19956 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 92
ID ADB13268 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 93
ID ABO43346 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 94
ID ABO19701 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 95
ID ADA12595 standard; protein; 260 AA.
DE Human secreted/transmembrane polypeptide PRO322.
PN US2003055216-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 96
ID ADA74522 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 97
ID ADB24755 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 98
ID ADA82279 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 99
ID ADA75242 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 100
ID ADA85320 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 101
ID ADA84768 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 102
ID ADB30024 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 103
ID ADA80552 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 104
ID ADA75794 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082703-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 105
ID ADA7019 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 106
ID ADB25315 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 107
ID ADA93491 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 108
ID ADB26841 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 109
ID ADB31128 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 110
ID ADA61056 standard; protein; 260 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 111
ID ADB24203 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 112
ID ADA96532 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 113
ID ADA81104 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 114
ID ADA95980 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 115
ID ADB26289 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 116
ID ADB1774 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 117
ID ABO19592 standard; protein; 260 AA.
DE Novel human secreted and transmembrane polypeptide #60.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 118
ID ADA77553 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 119
ID ADB18293 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 120
ID ADA86976 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 121
ID ADA88079 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 122
ID ADA6467 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

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RESULT 123
ID ADB8497 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US200308269-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 124
ID ADB29049 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 125
ID ADA77001 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 126
ID ADA8631 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 127
ID ADA97636 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 128
ID ADB27393 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 129
ID ADB2326 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 130
ID ADA67017 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 131
ID ADB22878 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 132
ID ADB3651 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003082764-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 133
ID ADA2373 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 134
ID ADB15436 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 135
ID ADB3868 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 136
ID ADB38136 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 137
ID ADB6608 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 138
ID ADB8968 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 139
ID ADB90420 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 140
ID ADB80561 standard; protein; 260 AA.
DE Ovarian cancer-associated protein #63.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (E0SB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
RESULT 141
ID ADB39521 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082764-A1.
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PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 142
ID ADB37901 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 143
ID ADB3714 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 144
ID ADB86751 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 145
ID ADB76617 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 146
ID ADB77356 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 147
ID ADB34513 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 148
ID ADB35617 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 149
ID ADB33961 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 150
ID ADB35065 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 151
ID ADB36169 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 152
ID ADB46564 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 153
ID ADC44043 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 154
ID ADC61803 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 155
ID ADC63767 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 156
ID ADC66867 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 157
ID ADC68991 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 158
ID ADC63051 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 159
ID ADC68116 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 178
ID ADC90213 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 179
ID ADC9632 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 180
ID ADC48521 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 181
ID ADD10050 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 182
ID ADD04625 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 183
ID ADC80581 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 184
ID ADD09100 standard; protein; 260 AA.
DE Human Kallikrein 8 protein SEQ ID NO:2.
PN WO2003085404-A1.
PD 16-OCT-2003.
PA (MCUN) MOUNT SINAI HOSPITAL.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 185
ID ADD11088 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 186
ID ADD10361 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 187

ID ADC47969 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 188
ID ADC80029 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 189
ID ADD11321 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 190
ID ADD09498 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 191
ID ADD41211 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 192
ID ADD52350 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 193
ID ADD53090 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 194
ID ADD53642 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 195
ID ADD17114 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 196
ID ABW00074 standard; protein; 260 AA.

DE Human tumour antigen derived gene-14 (TADG-14) protein.
PN US2002037581-A1.
PD 28-MAR-2002.
PA (UMBR-) UMB RES FOUND.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 197
ID ADE51798 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 198
ID ADD02597 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 199
ID ADD02031 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 200
ID ADD54213 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 201
ID ADE49429 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 202
ID ADD92530 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 203
ID ADD91426 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 204
ID ADE04040 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 205
ID ADE32337 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 206
ID ADE22269 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 207
ID ADD79493 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 208
ID ADE35483 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 209
ID ADE16597 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 210
ID ADD73212 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 211
ID ADE42029 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 212
ID ADE17846 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 213
ID ADD91978 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 214
ID ADE33441 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194767-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 215
ID ADE33993 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 216
ID ADE00045 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 217
ID ADE93082 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 218
ID ADE72570 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 219
ID ADE19502 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 220
ID ADE18950 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 221
ID ADE43146 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 222
ID ADE05935 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 223
ID ADE2821 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 224
ID ADE78939 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 225
ID ADE32889 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 226
ID ADE42581 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 227
ID ADE17221 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 228
ID ADE080597 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 229
ID ADE89625 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 230
ID ADE40909 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 231
ID ADE04708 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 232
ID ADE92837 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

	Query Match	45.9%; Score 630.5; DB 7;	Length 260;
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 233		
ID	ADF47235 standard; protein; 260 AA.		
DE	Human secreted/transmembrane protein, PRO322.		
PN	US200319533-A1.		
PD	16-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 234		
ID	ADG21546 standard; protein; 260 AA.		
DE	Novel human secreted and transmembrane protein PRO322.		
PN	US2003207355-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 235		
ID	ADG23187 standard; protein; 260 AA.		
DE	Novel human secreted and transmembrane protein PRO322.		
PN	US2003207384-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 236		
ID	ADF97522 standard; protein; 260 AA.		
DE	Human PRO polypeptide #198.		
PN	US2003207370-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 237		
ID	ADG80586 standard; protein; 260 AA.		
DE	Human PRO polypeptide #198.		
PN	US2003207373-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 238		
ID	ADGS2992 standard; protein; 260 AA.		
DE	Human secreted/transmembrane protein, PRO322.		
PN	US2003216561-A1.		
PD	20-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 239		
ID	ADG60312 standard; protein; 260 AA.		
DE	Human secreted/transmembrane protein, PRO322.		
PN	US2003206915-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 240		
ID	ADG80034 standard; protein; 260 AA.		
DE	Human PRO polypeptide #198.		
PN	US2003207372-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 241		
ID	ADHS5326 standard; protein; 260 AA.		
DE	Novel human secreted and transmembrane protein PRO322.		
PN	US2003207381-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 241		
ID	ADHS5326 standard; protein; 260 AA.		
DE	Novel human secreted and transmembrane protein PRO322.		
PN	US2003207381-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 241		
ID	ADHS5326 standard; protein; 260 AA.		
DE	Novel human secreted and transmembrane protein PRO322.		
PN	US2003207381-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 241		
ID	ADHS5326 standard; protein; 260 AA.		
DE	Novel human secreted and transmembrane protein PRO322.		
PN	US2003207381-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 241		
ID	ADHS5326 standard; protein; 260 AA.		
DE	Novel human secreted and transmembrane protein PRO322.		
PN	US2003207381-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	45.9%; Score 630.5; DB 7;	Length 260;	
ID	Best Local Similarity	50.2%; Pred. No. 1.1e-40;	
PID	RESULT 241		
ID	ADHS5326 standard; protein; 260 AA.		
DE	Novel human secreted and transmembrane protein PRO322.		

Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 242		
ID ADH55678 standard; protein; 260 AA.		
DE Novel human secreted and transmembrane protein PRO322.		
PN US2003207379-A1.		
PD 06-NOV-2003.		
PA (GETH) GENENTECH INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 243		
ID ADI61072 standard; protein; 260 AA.		
DE Human secreted/transmembrane protein, PRO322.		
PN US2003077700-A1.		
PD 24-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 244		
ID ADI64097 standard; protein; 260 AA.		
DE Novel human secreted and transmembrane protein PRO322.		
PN US2003077385-A1.		
PD 06-NOV-2003.		
PA (GETH) GENENTECH INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 245		
ID ADH81959 standard; protein; 260 AA.		
DE Novel human secreted and transmembrane protein PRO322.		
PN US2003207388-A1.		
PD 06-NOV-2003		
PA (GETH) GENENTECH INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 246		
ID ADH81407 standard; protein; 260 AA.		
DE Novel human secreted and transmembrane protein PRO322.		
PN US2003207377-A1.		
PD 06-NOV-2003.		
PA (GETH) GENENTECH INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 247		
ID ADH82576 standard; protein; 260 AA.		
DE Novel human secreted and transmembrane protein PRO322.		
PN US2003087355-A1.		
PD 08-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 248		
ID ADN15975 standard; protein; 260 AA.		
DE Novel human secreted and transmembrane protein PRO322.		
PN US2000108753-A1.		
PD 08-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 249		
ID ADN16604 standard; protein; 260 AA.		
DE Novel human secreted and transmembrane protein PRO322.		
PN US2003087385-A1.		
PD 08-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 250		
ID ADN35182 standard; protein; 260 AA.		
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.		
PN WO2003046661-A2.		
PD 22-MAY-2003.		
PA (BOSB-) BOS BIOTECHNOLOGY INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;
RESULT 251		
ID ADN35182 standard; protein; 260 AA.		
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.		
PN WO2003046661-A2.		
PD 22-MAY-2003.		
PA (BOSB-) BOS BIOTECHNOLOGY INC.		
Query Match	45.9%;	Score 630.5; DB 7; Length 260;
Best Local Similarity	50.2%;	Pred. No. 1.1e-40;


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RESULT 251
ID ADN15423 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 252
ID ADN14671 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 253
ID AD165046 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 254
ID AD163545 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 255
ID ADC81133 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 256
ID ADD76581 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 257
ID ADD87945 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 258
ID ADD86349 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 259
ID ADE875797 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 260
ID ADE89830 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 261
ID ADE41322 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 262
ID ADE23373 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 263
ID ADE23925 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 264
ID ADE24568 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 265
ID ADD87393 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 266
ID ADE89259 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 267
ID ADE18398 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 268
ID ADE88707 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 269
ID ADE89830 standard; protein; 260 AA.
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DE Human secreted/transmembrane protein, PRO322.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOSTEIN D.
PA (DESN/) DESNOYERS L.
PA (BATO/) BATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROWM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 270
ID ADF61470 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 271
ID ADF40162 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 272
ID ADF45958 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 273
ID ADF94727 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 274
ID ADF91138 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 275

ID ADF95279 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 276
ID ADF93389 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 277
ID ADF24354 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 278
ID ADF40786 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003198021-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 279
ID ADF23730 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 280
ID ADF33713 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 281
ID ADF34970 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 282
ID ADF27180 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 283
ID ADF27816 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH/) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 284
ID ADF92285 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein PRO322.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 285
ID ADE90586 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 286
ID ADF41410 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 287
ID ADF33089 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 288
ID ADF25455 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 289
ID ADF26556 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 290
ID ADF34345 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 291
ID ADF46582 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 292
ID ADE91733 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 293
ID ADF02312 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 294
ID ADF98074 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 295
ID ADF98074 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 296
ID ADF98074 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 297
ID ADF98074 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 298
ID ADF98645 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 299
ID ADF98645 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 300
ID ADF99197 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 301
ID ADF16782 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 302
ID ADF05241 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207375-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 303
ID ADG19508 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 304
ID ADG1345 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 305
ID ADG08402 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 306
ID ADG15572 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 307
ID ADG6970 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 308
ID ADG06155 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 309
ID ADG23739 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 310
ID ADG04028 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 311
ID ADG24929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 312
ID ADG07226 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 313
ID ADG07778 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 314
ID ADG5573 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 315
ID ADG60937 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 316
ID ADG62041 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 317
ID ADG82242 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 318
ID ADG57481 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 319
ID ADG56929 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 320
ID ADG55825 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 321
ID ADG58585 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 322
ID ADG70951 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 323
ID ADG58033 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 324
ID ADG53617 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 325
ID ADG71503 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 326
ID ADG50568 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 327
ID ADG81690 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 328
ID ADH30652 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 329
ID ADH12019 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 330
ID ADG43944 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 331
ID ADG51816 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 332
ID ADG52441 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 333
ID ADG54169 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 334
ID ADG43320 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 335
ID ADG81138 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 336
ID ADG56377 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 337
ID ADH12643 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 338
ID ADG48696 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 339

ID ADG61489 standard; protein; 260 AA.
 DE Novel human secreted and transmembrane protein PRO322.
 PN US2003207429-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 340
 ID ADH28576 standard; protein; 260 AA.
 DE Human PRO polypeptide #198.
 PN US2003022331-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 341
 ID ADG54721 standard; protein; 260 AA.
 DE Novel human secreted and transmembrane protein PRO322.
 PN US2003207367-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 342
 ID ADG59761 standard; protein; 260 AA.
 DE Novel human secreted and transmembrane protein PRO322.
 PN US2003207369-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 343
 ID ADG51192 standard; protein; 260 AA.
 DE Human secreted/transmembrane protein, PRO322.
 PN US2004005312-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 344
 ID ADH43505 standard; protein; 260 AA.
 DE Human PRO polypeptide #36.
 PN US200324984-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 345
 ID ADG59136 standard; protein; 260 AA.
 DE Human secreted/transmembrane protein, PRO322.
 PN US2004005657-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 346
 ID ADG62592 standard; protein; 260 AA.
 DE Human secreted/transmembrane protein, PRO322.
 PN US2004006219-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 347
 ID ADI81185 standard; protein; 260 AA.
 DE Human PRO polypeptide #198.
 PN US2003207361-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 348
 ID ADI39730 standard; protein; 260 AA.

DE Human TADG-14 protein.
 PN US6642013-B1.
 PD 04-NOV-2003.
 PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 349
 ID ADH25617 standard; protein; 260 AA.
 DE Human neurotrophin homologue related protein sequence SEQ ID NO:395.
 PN EP1386931-A1.
 PD 04-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 350
 ID ADG09928 standard; protein; 260 AA.
 DE Novel human secreted and transmembrane protein PRO322.
 PN US2004009548-A1.
 PD 15-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 351
 ID ADI15399 standard; protein; 260 AA.
 DE Novel human secreted and transmembrane protein PRO322.
 PN US2003207382-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 352
 ID ADG09276 standard; protein; 260 AA.
 DE Novel human secreted and transmembrane protein PRO322.
 PN US2004009547-A1.
 PD 15-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 353
 ID ADI14731 standard; protein; 260 AA.
 DE Novel human secreted and transmembrane protein PRO322.
 PN US2003207383-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 354
 ID ADI18326 standard; protein; 260 AA.
 DE Novel human secreted and transmembrane protein PRO322.
 PN US2003207349-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 355
 ID ADI37154 standard; protein; 260 AA.
 DE Human TADG-14 protein.
 PN US2003199010-A1.
 PD 23-OCT-2003.
 PA (UYAR-) UNIV ARKANSAS.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 356
 ID ADG63607 standard; protein; 260 AA.
 DE Novel human secreted and transmembrane protein PRO322.
 PN US2004039164-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 45.9%; Score 630.5; DB 8; Length 260;
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;
 RESULT 357
 ID ADI77502 standard; protein; 260 AA.
 DE Human PRO polypeptide #198.

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PN  US2004038336-A1.
PD  26-FEB-2004.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 358
ID  ADK82850 standard; protein; 260 AA.
DE  Human PRO polypeptide #36.
PN  US200403927-A1.
PD  04-MAR-2004.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 359
ID  ADJ5624 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2004038335-A1.
PD  26-FEB-2004.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 360
ID  ADM27760 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2004048333-A1.
PD  11-MAR-2004.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 361
ID  ADM17394 standard; protein; 260 AA.
DE  Human secreted/transmembrane protein, PRO322.
PN  US2004048332-A1.
PD  11-MAR-2004.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 362
ID  ADL07228 standard; protein; 260 AA.
DE  Human secreted/transmembrane protein, PRO322.
PN  US2004063921-A1.
PD  01-APR-2004.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 363
ID  ADM42484 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2004058424-A1.
PD  25-MAR-2004.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 364
ID  ADM62866 standard; protein; 260 AA.
DE  Human NOV11h.
PN  US2004038223-A1.
PD  26-FEB-2004.
PA  (SMIT/) SMITHSON G.
PA  (MILL/) MILLET I.
PA  (PEWM/) PEWMAN J A.
PA  (KEKU/) KEKUDA R.
PA  (JUUU/) JU J.
PA  (LILL/) LI L.
PA  (GUOX/) GUO X.
PA  (PATU/) PATURAJAN M.
PA  (SPYT/) SPYTEK K A.
PA  (EDIN/) EDINGER S R.
PA  (ELLE/) ELTERMAN K.
PA  (MALY/) MALYANKAR V M.
PA  (ORTT/) ORT T.
PA  (GORM/) GORMAN L.
PA  (ZERH/) ZERHUSEN B D.

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PA  (ANDE/) ANDERSON D W.
PA  (ZHON/) ZHONG M.
PA  (CATY/) CATTERTON E.
PA  (CIWM/) CI W.
PA  (MILL/) MILLER C E.
PA  (RAST/) RASTELI L.
PA  (STON/) STONE D J.
PA  (PENA/) PENA C E A.
PA  (SHEN/) SHENOY S G.
PA  (SHIM/) SHIMKETS R A.
PA  (ROTH/) ROTHENBERG M E.
PA  (LEAC/) LEACH M D.
PA  (AGEE/) AGEER M L.
PA  (BERG/) BERGHS C.
PA  (DIRP/) DIRIPO V A.
PA  (EISE/) EISEN A.
PA  (GANG/) GANGOLLI E A.
PA  (RIEG/) RIEGER D K.
PA  (SPAD/) SPADERNA S K.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 365
ID  ADN04214 standard; protein; 260 AA.
DE  Antipsoriatic protein sequence #302.
PN  WO2004028479-A2.
PD  08-APR-2004.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 366
ID  ADM28346 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2004077064-A1.
PD  22-APR-2004.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 367
ID  ADI95828 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003077659-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 368
ID  ADI96380 standard; protein; 260 AA.
DE  Novel human secreted and transmembrane protein PRO322.
PN  US2003207354-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 369
ID  ADR72883 standard; protein; 260 AA.
DE  Human ovarian cancer-related tumour marker kallikrein 8 (bK8) protein.
PN  WO2004075713-A2.
PD  10-SEP-2004.
PA  (MOUN/) MOUNT SINAI HOSPITAL.
Query Match          45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 370
ID  AAY32853 standard; protein; 305 AA.
DE  Human serine protease protein sequence.
PN  JP1125765-A.
PD  24-AUG-1999.
PA  (SUNR/) SUNTORY LTD.
Query Match          45.6%; Score 627; DB 2; Length 305;
Best Local Similarity 50.9%; Pred. No. 2.4e-40;
RESULT 371
ID  AAB37985 standard; protein; 306 AA.
DE  Human secreted protein encoded by gene 2 clone HWJAB49.
PN  WO200055371-A1.

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PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.6%; Score 627; DB 3; Length 306;
Best Local Similarity 50.9%; Pred. No. 2.4e-40;
RESULT 372
ID ABB41332 standard; protein; 315 AA.
DE Human ovarian antigen HCOOP78, SEQ ID NO:2464.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.6%; Score 627; DB 5; Length 315;
Best Local Similarity 50.9%; Pred. No. 2.4e-40;
RESULT 373
ID AAW87703 standard; protein; 260 AA.
DE A human serine protease designated HGBAB90.
PN EP887414-A2.
PD 30-DEC-1998.
PA (SMK-) SMITHKLINE BEECHAM PLC.
Query Match 45.6%; Score 626.5; DB 2; Length 260;
Best Local Similarity 50.4%; Pred. No. 2.2e-40;
RESULT 374
ID AAB21311 standard; protein; 275 AA.
DE Human neuropsin.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN-) MOUNT SINAI HOSPITAL.
Query Match 45.6%; Score 626.5; DB 3; Length 275;
Best Local Similarity 50.4%; Pred. No. 2.3e-40;
RESULT 375
ID AAW10694 standard; protein; 260 AA.
DE Human recombinant neuropsin, used for antibody production.
PN JP08245700-A.
PD 24-SEP-1996.
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
Query Match 45.3%; Score 622.5; DB 2; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 376
ID AAW12393 standard; protein; 260 AA.
DE Mouse neuropsin protein.
PN JP08311099-A.
PD 26-NOV-1996.
PA (SHIO-) SHIOZAKA S.
Query Match 45.3%; Score 622.5; DB 2; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 377
ID AAY06438 standard; protein; 260 AA.
DE Human protease HUPW-7.
PN WO9936550-A2.
PD 22-JUL-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 45.3%; Score 622.5; DB 2; Length 260;
Best Local Similarity 49.8%; Pred. No. 4.5e-40;
RESULT 378
ID ABB57219 standard; protein; 260 AA.
DE Mouse ischemic condition related protein sequence SEQ ID NO:533.
PN WO20018188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NITHON SCHOOL JURIDICAL PERSON.
Query Match 45.3%; Score 622.5; DB 5; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 379
ID ADI17073 standard; protein; 260 AA.
DE Murine NOVX protein homologue SegID 609.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.3%; Score 622.5; DB 5; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 380
ID ADI39731 standard; protein; 260 AA.
DE Mouse neuropsin protein.
PN US642013-B1.
PD 04-NOV-2003.

PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Query Match 45.3%; Score 622.5; DB 8; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 381
ID ADI37155 standard; protein; 260 AA.
DE Mouse neuropsin.
PN US2003198010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Query Match 45.3%; Score 622.5; DB 8; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 382
ID ADI17074 standard; protein; 260 AA.
DE Rat NOVX protein homologue SegID 610.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.2%; Score 621.5; DB 5; Length 260;
Best Local Similarity 48.6%; Pred. No. 5.3e-40;
RESULT 383
ID AAB21325 standard; protein; 250 AA.
DE Human TUSP.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN-) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 3; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 384
ID AAY93390 standard; protein; 250 AA.
DE Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 3; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 385
ID AAB6139 standard; protein; 250 AA.
DE Protein of the invention #51.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH-) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 4; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 386
ID AAU12424 standard; protein; 250 AA.
DE Human PRO1279 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH-) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 4; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 387
ID ABB50479 standard; protein; 250 AA.
DE Human secreted protein encoded by gene 179 SEQ ID NO:427.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.0%; Score 618.5; DB 4; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 388
ID AAV83684 standard; protein; 250 AA.
DE Human PRO protein, Seq ID No 186.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH-) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 5; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 389
ID ABB61816 standard; protein; 250 AA.
DE Prostate cancer-associated protein #17.
PN WO200230268-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 45.0%; Score 618.5; DB 5; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 390
ID ABB84920 standard; protein; 250 AA.
DE Human PRO1279 protein sequence SEQ ID NO:208.
PN W0200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 5; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 391
ID ABB95526 standard; protein; 250 AA.
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
PN W0200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLMAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.0%; Score 618.5; DB 5; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 392
ID ABO17868 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 393
ID ABU80831 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 394
ID ABO33797 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 395
ID ABU81122 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 396
ID ABUS6739 standard; protein; 250 AA.
DE lung cancer-associated polypeptide #332.
PN W0200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 397
ID ABUE6822 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 398
ID ABUS9903 standard; protein; 250 AA.
DE Novel secreted and transmembrane protein PRO1279.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 399
ID ABO25093 standard; protein; 250 AA.
DE Human secreted/transmembrane protein (PRO) #253.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 400
ID ABU82140 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 401
ID ABU67098 standard; protein; 250 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 506.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 402
ID ADA46025 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 403
ID ADA76456 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 404
ID ABU72320 standard; protein; 250 AA.
DE Human PRO1279 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 405
ID ADA19106 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 406

ID ADA61729 standard; protein; 250 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 407
ID ADB19514 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 408
ID ADB28055 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 409
ID ADA6534 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 410
ID ADB16098 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 411
ID ADA47684 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 412
ID ABO44736 standard; protein; 250 AA.
DE Novel human secreted protein #179.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 413
ID ABO33632 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 414
ID ADA67679 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068785-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 415
ID ADB30686 standard; protein; 250 AA.

DE Human PRO polypeptide #253.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 416
ID ADA85982 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 417
ID ADA97194 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 418
ID ADA79498 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 419
ID ADA87637 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 420
ID ADB16839 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 421
ID ADA91931 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 422
ID ADB14994 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 423
ID ADB18955 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 424
ID ADA94170 standard; protein; 250 AA.
DE Human PRO polypeptide #253.

PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 425
ID ADB20066 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 426
ID ADB13378 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 427
ID ABO43401 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 428
ID ADA74632 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 429
ID ADB24665 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 430
ID ADA82389 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 431
ID ADA75352 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 432
ID ADA85430 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 433
ID ADA84878 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082708-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 434
ID ADB30134 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 435
ID ADA80662 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 436
ID ADA75904 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 437
ID ADA47129 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 438
ID ADB25425 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 439
ID ADA93601 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 440
ID ADB26951 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US20030932147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 441
ID ADB31238 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003093686-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 442
ID ABU72448 standard; protein; 250 AA.
DE Human PRO1279 protein.
PN US2003027988-A1.
PD 06-FEB-2003.

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PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 443
ID ADA61166 standard; protein; 250 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 444
ID ADB24313 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 445
ID ADA96642 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 446
ID ADA81214 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 447
ID ADA96090 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 448
ID ADB26399 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 449
ID ADB21884 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 450
ID ABO34343 standard; protein; 250 AA.
DE Human secreted/transmembrane polypeptide PRO 1279.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 451
ID ADA77663 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 452
ID ADB18403 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 453
ID ADA87086 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 454
ID ABO44485 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 455
ID ADA88189 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 456
ID ADA46577 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 457
ID ADB28607 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 458
ID ADB29159 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 459
ID ABO26216 standard; protein; 250 AA.
DE Human protein from novel secreted protein gene 179.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 460
ID ADA77111 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 461
ID ABO33509 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 462
ID ADA88741 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 463
ID ADA97746 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 464
ID ADA97746 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 465
ID ADB22436 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 466
ID ABJ72150 standard; protein; 250 AA.
DE Human membrane bound receptor/protein PRO1279 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 467
ID ADA67127 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 468
ID ADB22988 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 469
ID ADB23761 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 470
ID ADA92483 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 471
ID ADB15546 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003083352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 472
ID ADB83676 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 473
ID ADB80782 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 474
ID ADB73323 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 475
ID ADB38798 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 476
ID ADB78405 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 477
ID ADB38246 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 478
ID ADB66718 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 479
ID ADB85053 standard; protein; 250 AA.
DE Human PRO polypeptide #93.

PN US2003073817-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 480
 ID ADB89798 standard; protein; 250 AA.
 DE Human PRO polypeptide #253.
 PN US2003082698-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 481
 ID ADB90530 standard; protein; 250 AA.
 DE Human PRO polypeptide #253.
 PN US2003082762-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 482
 ID ADB80596 standard; protein; 250 AA.
 DE Ovarian cancer-associated protein #81.
 PN WO2002102235-A2.
 PD 27-DEC-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 483
 ID ADB39631 standard; protein; 250 AA.
 DE Novel human secreted and transmembrane protein PRO1279.
 PN US2003082764-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 484
 ID ADB78159 standard; protein; 250 AA.
 DE Novel human secreted and transmembrane protein PRO1279.
 PN US2003092886-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 485
 ID ADB87225 standard; protein; 250 AA.
 DE Human PRO polypeptide #93.
 PN US2003088067-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 486
 ID ADB84807 standard; protein; 250 AA.
 DE Human PRO polypeptide #93.
 PN US2003092890-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 487
 ID ADB47254 standard; protein; 250 AA.
 DE Novel human secreted and transmembrane protein PRO1279.
 PN US2003082687-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 488
 ID ADB83922 standard; protein; 250 AA.
 DE Novel human secreted and transmembrane protein PRO1279.
 PN US2003069397-A1.

PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 489
 ID ADB86861 standard; protein; 250 AA.
 DE Human PRO polypeptide #253.
 PN US2003082697-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 490
 ID ADB73077 standard; protein; 250 AA.
 DE Novel human secreted and transmembrane protein PRO1279.
 PN US2003092887-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 491
 ID ADB77466 standard; protein; 250 AA.
 DE Novel human secreted and transmembrane protein PRO1279.
 PN US2003082696-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 492
 ID ADB75388 standard; protein; 250 AA.
 DE Prostate cancer marker protein.
 PN WO2003009814-A2.
 PD 06-FEB-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 493
 ID ADB34623 standard; protein; 250 AA.
 DE Human PRO polypeptide SEQ ID NO 506.
 PN US2003077717-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 494
 ID ADB35727 standard; protein; 250 AA.
 DE Human PRO polypeptide SEQ ID NO 506.
 PN US2003077719-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 495
 ID ADB34071 standard; protein; 250 AA.
 DE Human PRO polypeptide SEQ ID NO 506.
 PN US2003077716-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 496
 ID ADB35175 standard; protein; 250 AA.
 DE Human PRO polypeptide SEQ ID NO 506.
 PN US2003077718-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 45.0%; Score 618.5; DB 7; Length 250;
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 RESULT 497
 ID ADB36279 standard; protein; 250 AA.
 DE Human PRO polypeptide SEQ ID NO 506.
 PN US2003077720-A1.
 PD 24-APR-2003.

PA	(GETH) GENENTECH INC.	45.0%;	Score 618.5;	DB 7;	Length 250;
Query Match		48.2%;	Pred. No. 8.7e-40;		
Best Local Similarity					
RESULT 498					
ID	ADN46674 standard; protein; 250 AA.				
DE	Novel human secreted and transmembrane protein PRO1279.				
PN	US2003082692-A1.				
PD	01-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity		48.2%;	Pred. No. 8.7e-40;		
RESULT 499					
ID	ADC18039 standard; protein; 250 AA.				
DE	Human PRO polypeptide #51.				
PN	US2003064925-A1.				
PD	03-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity		48.2%;	Pred. No. 8.7e-40;		
RESULT 500					
ID	ADC36915 standard; protein; 250 AA.				
DE	Human PRO polypeptide #93.				
PN	US2003088065-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity		48.2%;	Pred. No. 8.7e-40;		
RESULT 501					
ID	ADC21905 standard; protein; 250 AA.				
DE	Human PRO polypeptide #93.				
PN	US2003096969-A1.				
PD	22-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity		48.2%;	Pred. No. 8.7e-40;		
RESULT 502					
ID	ADC50547 standard; protein; 250 AA.				
DE	Novel human secreted and transmembrane protein PRO1279.				
PN	US2003092106-A1.				
PD	15-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity		48.2%;	Pred. No. 8.7e-40;		
RESULT 503					
ID	ADC72094 standard; protein; 250 AA.				
DE	Novel human secreted and transmembrane protein PRO1279.				
PN	US2003092107-A1.				
PD	15-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity		48.2%;	Pred. No. 8.7e-40;		
RESULT 504					
ID	ADC60073 standard; protein; 250 AA.				
DE	Novel human secreted and transmembrane protein PRO1279.				
PN	US2003092105-A1.				
PD	15-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity		48.2%;	Pred. No. 8.7e-40;		
RESULT 505					
ID	ADC49936 standard; protein; 250 AA.				
DE	Novel human secreted and transmembrane protein PRO1279.				
PN	US2003088064-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity		48.2%;	Pred. No. 8.7e-40;		
RESULT 506					
ID	ADC49135 standard; protein; 250 AA.				
DE	Novel human secreted and transmembrane protein PRO1279.				
PN	US2003088070-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				

Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 507				
ID	ADC49652 standard; protein; 250 AA.			
ID	Novel human secreted and transmembrane protein PRO1279.			
PN	US2003088071-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 508				
ID	ADC47513 standard; protein; 250 AA.			
DE	Novel human secreted and transmembrane protein PRO1279.			
PN	US2003088072-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 509				
ID	ADC33080 standard; protein; 250 AA.			
DE	Novel human secreted and transmembrane protein Seg ID506.			
PN	US2003087365-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 510				
ID	ADC57434 standard; protein; 250 AA.			
DE	Novel human secreted and transmembrane protein Seg ID506.			
PN	US2003087366-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 511				
ID	ADC60625 standard; protein; 250 AA.			
ID	Novel human secreted and transmembrane protein PRO1279.			
PN	US2003087367-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 512				
ID	ADC51100 standard; protein; 250 AA.			
DE	Novel human secreted and transmembrane protein PRO1279.			
PN	US2003087361-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 513				
ID	ADC65627 standard; protein; 250 AA.			
DE	Human PRO polypeptide #253.			
PN	US2003087362-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 514				
ID	ADC54725 standard; protein; 250 AA.			
DE	Novel human secreted and transmembrane protein Seg ID506.			
PN	US2003087363-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 515				
ID	ADC53686 standard; protein; 250 AA.			
DE	Novel human secreted and transmembrane protein Seg ID506.			
PN	US2003087364-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 516				
ID	ADC53686 standard; protein; 250 AA.			
DE	Novel human secreted and transmembrane protein Seg ID506.			
PN	US2003087364-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;

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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 516
ID ADC59209 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 517
ID ADC56087 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 518
ID ADC58657 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein Seq ID506.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 519
ID ADC47258 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 520
ID ADD03331 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 521
ID ADC90323 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 522
ID ADC69742 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 523
ID ADC48631 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 524
ID ADD10160 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 525
ID AD78133 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 526
ID ADD04735 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 527
ID ADD06368 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 528
ID ADC80691 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 529
ID ADD1198 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 530
ID ADD10497 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 531
ID ADC48079 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 532
ID ADC77887 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 533
ID ADC80139 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 534
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ID ADD11457 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 535
ID ADD09608 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 536
ID ADD50850 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 537
ID ADD41321 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 538
ID ADD52460 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 539
ID ADD51096 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 540
ID ADD70685 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 541
ID ADD39762 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 542
ID ADD53200 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 543
ID ADD53752 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 544
ID ADD70208 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 545
ID ADD37250 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 546
ID ADD38329 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 547
ID ADD39285 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 548
ID ADD51908 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 549
ID ADD02707 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 550
ID ADD50577 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 551
ID ADD02141 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 552
ID ADD54323 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.

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PN US2003203432-A1.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 553
ID ADD50331 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 554
ID ADD38808 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 555
ID ADD40239 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 556
ID ADD51342 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 557
ID ADE50460 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 558
ID ADD92640 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 559
ID ADD91536 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 560
ID ADE04150 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 561
ID ADE20072 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 562
ID ADE32447 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 563
ID ADE22379 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 564
ID ADD79603 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 565
ID ADE42139 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 566
ID ADE17956 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 567
ID ADD92088 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 568
ID ADE33551 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 569
ID ADE34103 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 570
ID ADE80155 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207417-A1.
PD 06-NOV-2003.
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PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 571
ID ADE4983 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 572
ID ADD93192 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 573
ID ADE19612 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 574
ID ADE21541 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 575
ID ADE19060 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 576
ID ADE43256 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 577
ID ADE96045 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 578
ID ADE22931 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 579
ID ADD79049 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 580
ID ADE32999 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 581
ID ADE42691 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 582
ID ADD80707 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 583
ID ADD89735 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 584
ID ADE41019 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 585
ID ADE04818 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 586
ID ADE92947 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 587
ID ADF29966 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 588
ID ADF55859 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 589
ID ADE55859 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 589
ID ADG21656 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 590
ID ADG23297 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 591
ID ADP97632 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 592
ID ADG80696 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 593
ID ADG80144 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 594
ID ADH55436 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 595
ID ADH55988 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 596
ID ADH99363 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 597
ID ADI64207 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 598
ID ADI65156 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 599
ID ADH82069 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 600
ID ADH81517 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 601
ID ADM82686 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 602
ID ADN16085 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 603
ID ADN16714 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 604
ID ADN39242 standard; protein; 250 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:560.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 605
ID ADN15533 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 606
ID ADN14981 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 607

ID ADI63655 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 608
ID ADC4889 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 609
ID ADC81243 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 610
ID ADE21060 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 611
ID ADE05904 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 612
ID ADD76691 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 613
ID ADD75133 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 614
ID ADD75879 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 615
ID ADD8111 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 616
ID ADE46937 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 617
ID ADE20814 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 618
ID ADE39111 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 619
ID ADD88055 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 620
ID ADE86459 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 621
ID ADE05658 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 622
ID ADD73643 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 623
ID ADE75907 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 624
ID ADD78483 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 625
ID ADE41458 standard; protein; 250 AA.
DE Human secreted/transmembrane PRO polypeptide #104.

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PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 626
ID ADE23483 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 627
ID ADE21306 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 628
ID ADD77421 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 629
ID ADE20568 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 630
ID ADD75633 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 631
ID ADD74149 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 632
ID ADD74395 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 633
ID ADD76125 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 634
ID ADD85617 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100721-A1.
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PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 635
ID ADE24035 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 636
ID ADE24678 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 637
ID ADD87503 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 638
ID ADE05166 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 639
ID ADD75379 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 640
ID ADD76923 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 641
ID ADD86691 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 642
ID ADE89369 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 643
ID ADD78159 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100731-A1.
PD 29-MAY-2003.
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Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 653				
ID	ADBR05412 standard; protein;	250 AA.		
DE	Human PRO polypeptide #93.			
PN	US2003100723-A1.			
PD	29-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 654				
ID	AD074887 standard; protein;	250 AA.		
DE	Human PRO polypeptide #93.			
PN	US2003100724-A1.			
PD	29-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 655				
ID	ADBR6543 standard; protein;	250 AA.		
DE	Human secreted/transmembrane protein PRO1279.			
PN	US2003195347-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 656				
ID	ADBR4837 standard; protein;	250 AA.		
DE	Human PRO polypeptide #253.			
PN	US2003199027-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 657				
ID	ADBR1248 standard; protein;	250 AA.		
DE	Human PRO polypeptide #253.			
PN	US2003199061-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 658				
ID	ADFR25854 standard; protein;	250 AA.		
DE	Human secreted/transmembrane protein PRO1279.			
PN	US2003199675-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 659				
ID	ADBR5389 standard; protein;	250 AA.		
DE	Human PRO polypeptide #253.			
PN	US2003199052-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 660				
ID	ADBR3499 standard; protein;	250 AA.		
DE	Human PRO polypeptide #253.			
PN	US2003199060-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 661				
ID	ADFR4753 standard; protein;	250 AA.		
DE	Human secreted/transmembrane protein PRO1279.			
PN	US2003198993-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 662				
ID	ADBR1248 standard; protein;	250 AA.		
DE	Human PRO polypeptide #253.			
PN	US2003199061-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 663				
ID	ADBR05412 standard; protein;	250 AA.		
DE	Human PRO polypeptide #93.			
PN	US2003100723-A1.			
PD	29-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 664				
ID	AD074887 standard; protein;	250 AA.		
DE	Human PRO polypeptide #93.			
PN	US2003100724-A1.			
PD	29-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	45.0%;	Score 618.5;	DB 8;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 665				
ID	ADBR6543 standard; protein;	250 AA.		
DE	Human secreted/transmembrane protein PRO1279.			
PN	US2003195347-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			

Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 662
ID ADF29489 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 663
ID ADF35080 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 664
ID ADE97020 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 665
ID ADE92395 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 666
ID ADE90696 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 667
ID ADE91843 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 668
ID ADG05699 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 669
ID ADG27253 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 670
ID ADG02422 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 671

RESULT 671
ID ADG22028 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 672
ID ADG20278 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 673
ID ADF98184 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 674
ID ADG24401 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 675
ID ADF98755 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 676
ID ADG03586 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 677
ID ADF99307 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 678
ID ADG16892 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 679
ID ADG05351 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 680

ID ADG19618 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 681
ID ADG11316 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 682
ID ADG13455 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 683
ID ADG08512 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 684
ID ADG15682 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 685
ID ADG12095 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 686
ID ADP97080 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 687
ID ADG06265 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 688
ID ADG23849 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 689
ID ADG04138 standard; protein; 250 AA.

DE Human PRO polypeptide #253.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 690
ID ADG25039 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 691
ID ADP94652 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 692
ID ADG07336 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 693
ID ADG07888 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 694
ID ADG06748 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 695
ID ADG55383 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 696
ID ADG61047 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 697
ID ADG62151 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 698
ID ADH03058 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.

PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 699
ID ADG82352 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 700
ID ADG57591 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 701
ID ADG57039 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 702
ID ADG55935 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 703
ID ADG58695 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 704
ID ADG71061 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 705
ID ADH04012 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 706
ID ADH03535 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 707
ID ADH39092 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096965-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 708
ID ADG58143 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 709
ID ADG53727 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 710
ID ADG71613 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 711
ID ADG81800 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 712
ID ADH30762 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 713
ID ADH12129 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 714
ID ADG52551 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 715
ID ADG54279 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 716
ID ADG81248 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

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Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 717
ID ADG56487 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 718
ID ADH12753 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 719
ID ADG61599 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 720
ID ADH28686 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 721
ID ADG54831 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 722
ID ADG59871 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 723
ID ADH43641 standard; protein; 250 AA.
DE Human PRO polypeptide #104.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 724
ID ADG31482 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 725
ID ADH04489 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 726
ID ADH1295 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 727
ID ADI33652 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 728
ID ADH69746 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 729
ID ADH61490 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 730
ID ADG10038 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 731
ID ADI15509 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 732
ID ADG09386 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 733
ID ADI14841 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 734
ID ADI29907 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
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RESULT 735
ID AD18436 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 736
ID ADM27304 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 737
ID ADJ63717 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 738
ID ADJ77612 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 739
ID ADK82986 standard; protein; 250 AA.
DE Human PRO polypeptide #104.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 740
ID ADK66662 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 741
ID ADJ65734 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 742
ID ADM27870 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 743
ID ADM42594 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 744

ID ADL94689 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 745
ID ADM28456 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US200407064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 746
ID ADI95938 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US200307659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 747
ID ADI96490 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 748
ID ADR72632 standard; protein; 250 AA.
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 749
ID ADR72890 standard; protein; 250 AA.
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein2.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 750
ID ADS34892 standard; protein; 250 AA.
DE Human autoimmune disease-related protein - SEQ ID NO:2.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 751
ID AAY42439 standard; protein; 282 AA.
DE CASB12 amino acid sequence.
PN WO9949055-A1.
PD 30-SEP-1999.
PA (SMIT) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 45.0%; Score 618.5; DB 2; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 752
ID AAB11712 standard; protein; 282 AA.
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.
PN WO200031257-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 45.0%; Score 618.5; DB 3; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 753
ID AAY43636 standard; protein; 282 AA.

DE A human prostate-associated serum protease (PRASP).
PN W09941387-A2.
PD 19-AUG-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 45.0%; Score 618.5; DB 3; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 754
ID ADN11325 standard; protein: 282 AA.
DE Human kallikrein-11, marker for prostate cancer.
PN W02004029616-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 755
ID AD017587 standard; protein: 282 AA.
DE Human boar tissue sarcoma-upregulated protein - SEQ ID 404.
PN W02004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 756
ID AD872631 standard; protein: 282 AA.
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 1.
PN W02004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 757
ID AD872889 standard; protein: 282 AA.
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein1.
PN W02004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 758
ID ADS34693 standard; protein: 282 AA.
DE Human autoimmune disease-related protein - SEQ ID 107.
PN W02004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 45.0%; Score 618.5; DB 8; Length 282;
Best Local Similarity 48.2%; Pred. No. 9.9e-40;
RESULT 759
ID AAY42440 standard; protein: 281 AA.
DE CASB12 polypeptide derived from Expressed Sequence Tag products.
PN W09949055-A1.
PD 30-SEP-1999.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 44.6%; Score 612.5; DB 2; Length 281;
Best Local Similarity 48.0%; Pred. No. 2.8e-39;
RESULT 760
ID AAB36482 standard; protein: 288 AA.
DE Pusion gene with human serine protease catalytic domain protein #13.
PN W0200066709-A2.
PD 09-NOV-2000.
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.
Query Match 43.9%; Score 602.5; DB 3; Length 288;
Best Local Similarity 51.1%; Pred. No. 1.7e-38;
RESULT 761
ID AAB67542 standard; protein: 288 AA.
DE Amino acid sequence of catalytic domain in PFEK1-6XHS-TAG.
PN W0200116289-A2.
PD 08-MAR-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Query Match 43.9%; Score 602.5; DB 4; Length 288;
Best Local Similarity 51.1%; Pred. No. 1.7e-38;
RESULT 762
ID AAY36093 standard; protein: 250 AA.
DE Extended human secreted protein sequence, SEQ ID NO. 476.
PN W09931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 43.8%; Score 601.5; DB 2; Length 250;
Best Local Similarity 47.4%; Pred. No. 1.8e-38;
RESULT 763
ID ADP19401 standard; protein: 250 AA.
DE Human secreted polypeptide #252.
PN US200410939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 43.8%; Score 601.5; DB 8; Length 250;
Best Local Similarity 47.4%; Pred. No. 1.8e-38;
RESULT 764
ID AAB11714 standard; protein: 275 AA.
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO.6.
PN W0200031257-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 43.7%; Score 601; DB 3; Length 275;
Best Local Similarity 44.2%; Pred. No. 2.1e-38;
RESULT 765
ID AA082732 standard; protein: 320 AA.
DE Amino acid sequence of novel human protease #31.
PN W0200200860-A2.
PD 03-JAN-2002.
PA (SUG-) SUGEN INC.
Query Match 43.6%; Score 599.5; DB 5; Length 320;
Best Local Similarity 46.4%; Pred. No. 3.3e-38;
RESULT 766
ID AAE19166 standard; protein: 320 AA.
DE Human protease, PRIS-3 protein.
PN W0200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.6%; Score 599.5; DB 5; Length 320;
Best Local Similarity 46.4%; Pred. No. 3.3e-38;
RESULT 767
ID AD117075 standard; protein: 225 AA.
DE Murine NOVX protein homologue Segid 611.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 43.6%; Score 599; DB 5; Length 225;
Best Local Similarity 49.8%; Pred. No. 2.5e-38;
RESULT 768
ID AAU79390 standard; protein: 256 AA.
DE Novel human kallikrein KLK15.
PN W0200214485-A2.
PD 21-FEB-2002.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 43.6%; Score 599; DB 5; Length 256;
Best Local Similarity 47.1%; Pred. No. 2.8e-38;
RESULT 769
ID ADN10932 standard; protein: 256 AA.
DE Human kallikrein 15, marker of endocrine cancer.
PN W02004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 43.6%; Score 599; DB 8; Length 256;
Best Local Similarity 47.1%; Pred. No. 2.8e-38;
RESULT 770
ID AAB36483 standard; protein: 289 AA.
DE Fusion gene with human serine protease catalytic domain protein #14.
PN W0200066709-A2.
PD 09-NOV-2000.
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.
Query Match 43.6%; Score 598.5; DB 3; Length 289;
Best Local Similarity 49.1%; Pred. No. 3.5e-38;
RESULT 771
ID AAB67543 standard; protein: 289 AA.
DE Amino acid sequence of catalytic domain in PFEK1-6XHS-TAG.
PN W0200116289-A2.

PD 08-MAR-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Query Match 43.6%; Score 598.5; DB 4; Length 289;
Best Local Similarity 49.1%; Pred. No. 3.5e-38;
RESULT 772
ID AAE08017 standard; protein; 248 AA.
DE Human PS133 consensus protein sequence.
PN US6232456-B1.
PD 15-MAY-2001.
PA (ABBO) ABBOTT LAB.
Query Match 43.5%; Score 597.5; DB 4; Length 248;
Best Local Similarity 47.8%; Pred. No. 3.6e-38;
RESULT 773
ID AAB11713 standard; protein; 276 AA.
DE Mouse serine protease BSSP6 (MBSSP6) SEQ ID NO:4.
PN W0200031257-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 43.5%; Score 597.5; DB 3; Length 276;
Best Local Similarity 47.0%; Pred. No. 4e-38;
RESULT 774
ID ADC31389 standard; protein; 298 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1471.
PN W02003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 43.3%; Score 595; DB 7; Length 298;
Best Local Similarity 48.1%; Pred. No. 6.8e-38;
RESULT 775
ID AD117077 standard; protein; 260 AA.
DE Human NOVX protein homologue SeqID 613.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 43.2%; Score 593.5; DB 5; Length 260;
Best Local Similarity 48.6%; Pred. No. 7.7e-38;
RESULT 776
ID AAB21312 standard; protein; 228 AA.
DE Human TLSP.
PN W0200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 43.1%; Score 592; DB 3; Length 228;
Best Local Similarity 49.3%; Pred. No. 8.7e-38;
RESULT 777
ID AAN08475 standard; protein; 247 AA.
DE Porcine trypsinogen.
PN W09700316-A1.
PD 03-JAN-1997.
PA (NOVO) NOVO-NORDISK AS.
Query Match 41.7%; Score 573; DB 2; Length 247;
Best Local Similarity 45.6%; Pred. No. 2.8e-36;
RESULT 778
ID ABB98258 standard; protein; 247 AA.
DE Pig trypsinogen SEQ ID NO 1.
PN W0200261064-A2.
PD 08-AUG-2002.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
Query Match 41.7%; Score 573; DB 5; Length 247;
Best Local Similarity 45.6%; Pred. No. 2.8e-36;
RESULT 779
ID ADJ92132 standard; protein; 247 AA.
DE Pig pro-trypsin.
PN US2004043455-A1.
PD 04-MAR-2004.
PA (NOVO) NOVOZYMES BIOTECH INC.
Query Match 41.7%; Score 573; DB 8; Length 247;
Best Local Similarity 45.6%; Pred. No. 2.8e-36;
RESULT 780
ID AAB21306 standard; protein; 251 AA.
DE Human KLK-L6 protein #2.
PN W0200053776-A2.

PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.4%; Score 569.5; DB 3; Length 251;
Best Local Similarity 46.9%; Pred. No. 5.2e-36;
RESULT 781
ID ADN10930 standard; protein; 251 AA.
DE Human kallikrein 14, marker of endocrine cancer.
PN W02004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.4%; Score 569.5; DB 8; Length 251;
Best Local Similarity 46.9%; Pred. No. 5.2e-36;
RESULT 782
ID ABJ26666 standard; protein; 267 AA.
DE Human protein modification + maintenance molecule protein SEQ ID NO 20.
PN W02003000844-A2.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 41.4%; Score 569.5; DB 6; Length 267;
Best Local Similarity 46.9%; Pred. No. 5.6e-36;
RESULT 783
ID AAB21298 standard; protein; 250 AA.
DE Human KLK-L3 protein #2.
PN W0200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.4%; Score 568.5; DB 3; Length 250;
Best Local Similarity 46.7%; Pred. No. 6.2e-36;
RESULT 784
ID ABP64969 standard; protein; 250 AA.
DE Human novel SEQ ID 629.
PN W0200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
Query Match 41.4%; Score 568.5; DB 5; Length 250;
Best Local Similarity 46.7%; Pred. No. 6.2e-36;
RESULT 785
ID ABR55400 standard; protein; 250 AA.
DE Amino acid sequence of human kallikrein 9 (HK9).
PN W02003033731-A2.
PD 24-APR-2003.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.4%; Score 568.5; DB 6; Length 250;
Best Local Similarity 46.7%; Pred. No. 6.2e-36;
RESULT 786
ID ADN05516 standard; protein; 250 AA.
DE Antipsoriatic protein sequence #924.
PN W02004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 41.4%; Score 568.5; DB 8; Length 250;
Best Local Similarity 46.7%; Pred. No. 6.2e-36;
RESULT 787
ID AAB21300 standard; protein; 277 AA.
DE Human KLK-L4 protein #2.
PN W0200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.3%; Score 567; DB 3; Length 277;
Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 788
ID ABO00554 standard; protein; 277 AA.
DE Novel human polypeptide #141.
PN W02003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 41.3%; Score 567; DB 6; Length 277;
Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 789
ID ADJ1094 standard; protein; 277 AA.
DE Human kallikrein 13 protein SEQ ID NO:1.
PN W02004021009-A2.
PD 11-MAR-2004.

PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.1%; Score 567; DB 8; Length 277;
Best Local Similarity 46.8%; Pred. NO. 9e-36;
RESULT 790
ID ADN04184 standard; protein; 277 AA.
DE Antipeptidic protein sequence #287.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 41.3%; Score 567; DB 8; Length 277;
Best Local Similarity 46.8%; Pred. NO. 9e-36;
RESULT 791
ID ADRI4575 standard; protein; 277 AA.
DE Human NF-kappaB pathway-associated protein SeqID576.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 41.3%; Score 567; DB 8; Length 277;
Best Local Similarity 46.8%; Pred. NO. 9e-36;
RESULT 792
ID AAU16971 standard; protein; 251 AA.
DE Human novel secreted protein, SEQ ID 212.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.2%; Score 566.5; DB 4; Length 251;
Best Local Similarity 46.9%; Pred. NO. 8.9e-36;
RESULT 793
ID AAU23217 standard; protein; 247 AA.
DE Novel human enzyme polypeptide #303.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 4; Length 247;
Best Local Similarity 46.9%; Pred. NO. 1.3e-35;
RESULT 794
ID AAY16777 standard; protein; 293 AA.
DE Human keratinocyte derived protease (KDP).
PN WO9918219-A1.
PD 15-APR-1999.
PA (PROOC) PROCTER & GAMBLE CO.
Query Match 41.1%; Score 564.5; DB 2; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 795
ID AAY30524 standard; protein; 293 AA.
DE Human PDSP-1 protein.
PN WO9946391-A2.
PD 16-SEP-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 41.1%; Score 564.5; DB 2; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 796
ID AAY38412 standard; protein; 293 AA.
DE Human secreted protein encoded by gene No. 27.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 2; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 797
ID AAY38426 standard; protein; 293 AA.
DE Human secreted protein encoded by gene No. 27.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 2; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 798
ID AAY66726 standard; protein; 293 AA.
DE Membrane-bound protein PRO1132.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 3; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 799
ID AAB21296 standard; protein; 293 AA.
DE Human KIK-L2 protein.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.1%; Score 564.5; DB 3; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 800
ID AAU12399 standard; protein; 293 AA.
DE Human PRO1132 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 4; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 801
ID AAB65249 standard; protein; 293 AA.
DE Human PRO1132 (UNQ570) protein sequence SEQ ID NO.309.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 4; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 802
ID AAU81966 standard; protein; 293 AA.
DE Human PRO1132.
PN WO200109327-A2.
PD 08-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 5; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 803
ID ABUS8064 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 804
ID ABUS9142 standard; protein; 293 AA.
DE Novel human secreted or transmembrane protein PRO1132.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 805
ID ABU82654 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 806
ID ABO17843 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 807
ID ADA57425 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 808

ID ADA56974 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 809
ID ADA57427 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 810
ID ADA57428 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 811
ID ABU60573 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, #130.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 812
ID ABU13955 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 813
ID ABU81097 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 814
ID ABU72540 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 815
ID ABU66797 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 816
ID ADA41303 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 817
ID ADA41305 standard; protein; 293 AA.

DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 818
ID ADA40825 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 819
ID ADA41306 standard; protein; 293 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 820
ID ABUS9878 standard; protein; 293 AA.
DE Novel secreted and transmembrane protein PRO1132.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 821
ID ABUS9289 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, #130.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 822
ID ABO25986 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 823
ID ABO25068 standard; protein; 293 AA.
DE Human secreted/transmembrane protein (PRO) #228.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 824
ID ABUS8995 standard; protein; 293 AA.
DE Human secreted/transmembrane protein, #130.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 825
ID ABU92373 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 826
ID ABUS9438 standard; protein; 293 AA.
DE Novel human secreted or transmembrane protein PRO1346.
PN US2003027985-A1.
PD 06-FEB-2003.


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Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 827
ID ABL67073 standard; protein: 293 AA.
DE Human secreted/cranmembrane, PRO, protein SEQ ID 456.
PN US200303215-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 828
ID ABL92204 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 829
ID ABL10910 standard; protein: 293 AA.
DE Human PRO polypeptide #96.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 830
ID ABL81662 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 831
ID ABL88601 standard; protein: 293 AA.
DE Human secreted and transmembrane polypeptide PRO1132.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 832
ID ABL34115 standard; protein: 293 AA.
DE Human PRO1132 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 833
ID ADA45975 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 834
ID ADA76406 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 835
ID ADA19056 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 836
ID ADA61679 standard; protein: 293 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 837
ID ADA19464 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 838
ID ADA28005 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 839
ID ADA86484 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 840
ID ABL16048 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 841
ID ADA37820 standard; protein: 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 842
ID ADA47834 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 843
ID ADA21506 standard; protein: 293 AA.
DE Human secreted/cranmembrane polypeptide PRO1132.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 844
ID ADA10293 standard; protein: 293 AA.
DE Human secreted/cranmembrane protein, PRO1132.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      41.1% Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3% Pred. No. 1.5e-35;
RESULT 845
ID ADA67629 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003068795-A1.
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[illegible]

Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 855			
ID ADB14944 standard; protein; 293 AA.			
DE Human PRO polypeptide #228.			
PN US2003087351-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 856			
ID ADB18905 standard; protein; 293 AA.			
DE Novel human secreted and transmembrane protein PRO1132.			
PN US2003073211-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293;
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 857			
ID ADA94120 standard; protein; 293 AA.			
DE Human PRO polypeptide #228.			
PN US2003077722-A1.			
PD 24-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293;
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 858			
ID ADB20016 standard; protein; 293 AA.			
DE Novel human secreted and transmembrane protein PRO1132.			
PN US2003082691-A1.			
PD 01-MAY-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293;
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 859			
ID ADB13328 standard; protein; 293 AA.			
DE Human PRO polypeptide #228.			
PN US2003082710-A1.			
PD 01-MAY-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293;
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 860			
ID ABO43376 standard; protein; 293 AA.			
DE Novel human secreted and transmembrane protein PRO1132.			
PN US200304945-A1.			
PD 06-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293;
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 861			
ID ADA94525 standard; protein; 293 AA.			
DE Human secreted/transmembrane protein PRO1132.			
PN US2003059832-A1.			
PD 27-MAR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293;
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 862			
ID ADA74582 standard; protein; 293 AA.			
DE Human PRO polypeptide #228.			
PN US2003068798-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293;
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 863			
ID ADB24815 standard; protein; 293 AA.			
DE Human PRO polypeptide SEQ ID NO 456.			
PN US2003077713-A1.			
PD 24-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293;
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 864			
ID ADB24815 standard; protein; 293 AA.			
DE Human PRO polypeptide SEQ ID NO 456.			
PN US2003077713-A1.			
PD 24-APR-2003.			
PA (GETH) GENENTECH INC.			
Query Match	41.1%;	Score 564.5; DB 6;	Length 293;
Best Local Similarity	45.3%;	Pred. No. 1.5e-35;	
RESULT 864			

ID ADA82339 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 865
ID ADA75302 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 866
ID ADA85380 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 867
ID ADA84828 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 868
ID ADA830084 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 869
ID ADA80612 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 870
ID ADA75854 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 871
ID ADA38750 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 872
ID ADA47079 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 873
ID ADA25375 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.

PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 874
ID ADA93551 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 875
ID ADA26901 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 876
ID ADA31188 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 877
ID ADA92871 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 878
ID ADA61116 standard; protein; 293 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 879
ID ADB24263 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 880
ID ADA96592 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 881
ID ADA81164 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 882
ID ADA96040 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082759-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 883
ID ADB26349 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 884
ID ADB21834 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 885
ID ADA77613 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 886
ID ADB18353 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 887
ID ADA87036 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 888
ID ADA88139 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 889
ID ADA46527 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 890
ID ADB28557 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 891
ID ADB29109 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 892
ID ABO53201 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 893
ID ADA77061 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 894
ID ADA22432 standard; protein; 293 AA.
DE Human secreted/transmembrane polypeptide PRO1132.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 895
ID ADA86691 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 896
ID ADA97696 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 897
ID ADB27453 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 898
ID ADB22386 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 899
ID ABO22571 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 900
ID ADA06598 standard; protein; 293 AA.
DE Human secreted/transmembrane PRO polypeptide #96.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 901
ID ADA39291 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059782-A1.
PD 27-MAR-2003.

Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 902
ID ADB67077 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 903
ID ADB22938 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 904
ID ADB23711 standard; protein: 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 905
ID ADB92433 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 906
ID ADB15496 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 907
ID ADB38748 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 908
ID ADB96317 standard; protein: 293 AA.
DE Human PRO polypeptide #96.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 909
ID ADB38196 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 910
ID ADB66668 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

RESULT 911
ID ADB89748 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 912
ID ADB90480 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 913
ID ADB80490 standard; protein: 293 AA.
DE Ovarian cancer-associated protein #27.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (BOSB-) EOS BIOTECHNOLOGY INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 914
ID ADB39581 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 915
ID ADB47204 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 916
ID ADB86811 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 917
ID ADB7416 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 918
ID ADB34573 standard; protein: 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 919
ID ADB35677 standard; protein: 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 920

ID ADB34021 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADB35125 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADB36229 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADB46624 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US200308262-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC57789 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC55153 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC12020 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC56442 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC07497 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC11487 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;

RESULT 930
ID ADC50497 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC72044 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC60023 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC53030 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC57384 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC65075 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC51050 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC65577 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
ID ADC54675 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
RESULT 938
ID ADC54675 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
RESULT 939

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ID ADC53636 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 940
ID ADC59159 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 941
ID ADC56037 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 942
ID ADC58607 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 943
ID ADC14609 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 944
ID ADD08141 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 945
ID ADD03281 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 946
ID ADC90273 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 947
ID ADC81966 standard; protein: 293 AA.
DE Human PRO polypeptide #96.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 948
ID ADC69692 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 949
ID ADC48581 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 950
ID ADD10110 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 951
ID ADD07608 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 952
ID ADD04685 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 953
ID ADC82499 standard; protein: 293 AA.
DE Human PRO polypeptide #96.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 954
ID ADC80641 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 955
ID ADD1148 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 956
ID ADC48029 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 957
ID ADD08679 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
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RESULT 958
ID ADc80089 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 959
ID ADD06928 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 960
ID ADD09558 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 961
ID ADc83175 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 962
ID ADD41271 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 963
ID ADD52410 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 964
ID ADD53150 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 965
ID ADD53702 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 966
ID ADD55282 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 967
ID ADD56240 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 968
ID ADD51858 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 969
ID ADD02657 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 970
ID ADD02091 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 971
ID ADD54273 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 972
ID ADD54678 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 973
ID ADD92590 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 974
ID ADD91486 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 975
ID ADE04100 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
    Best Local Similarity 41.1%; Score 564.5; DB 7; Length 293;
    Pred. No. 1.5e-35;
RESULT 976
ID ADE26832 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087304-A1.
PD 08-MAY-2003.
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Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 977
ID ADE3297 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 978
ID ADE22329 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 979
ID ADD79553 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 980
ID ADE42089 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 981
ID ADE17906 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 982
ID ADD92038 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 983
ID ADE33501 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 984
ID ADE34053 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 985
ID ADD80105 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;

Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 986
ID ADD93142 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 987
ID ADE19562 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 988
ID ADE19010 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 989
ID ADE43206 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 990
ID ADD95995 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 991
ID ADE22881 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 992
ID ADD78999 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 993
ID ADE26299 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 994
ID ADE32949 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 995

ID ADE42641 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 996
ID ADD80657 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 997
ID ADD89685 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 998
ID ADE40969 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 999
ID ADE04768 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1000
ID ADE32897 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1001
ID ADE67236 standard; protein; 293 AA.
DE Human PRO1132 amino acid sequence SEQ ID NO:309.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1002
ID ADG21606 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1003
ID ADG23247 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1004
ID ADP97582 standard; protein; 293 AA.

DE Human PRO polypeptide #228.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1005
ID ADG80646 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1006
ID ADG80094 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1007
ID ADH5386 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1008
ID ADH55938 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1009
ID ADI35490 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1010
ID ADI64157 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1011
ID ADI65106 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1012
ID ADI63605 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1013
ID ADH82019 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207388-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1014
ID ADH9982 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1015
ID ADH81467 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1016
ID ADM82636 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1017
ID ADH16035 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1018
ID ADH16664 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1019
ID ADH39198 standard; protein; 293 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:516.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1020
ID ADH15483 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1021
ID ADH14931 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1022
ID ADC81193 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1023
ID ADD76641 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1024
ID ADD8005 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1025
ID ADD6409 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1026
ID ADE75857 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1027
ID ADE23433 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1028
ID ADE33985 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1029
ID ADE24628 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1030
ID ADD87453 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1031
ID ADE89319 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. NO. 1.5e-35;
RESULT 1032
ID ADE89319 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1032
ID ADE18458 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1033
ID ADE86767 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1034
ID ADE94787 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1035
ID ADE91198 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1036
ID ADF35435 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1037
ID ADE95339 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1038
ID ADE93449 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1039
ID ADF35030 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1040
ID ADE92345 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1041
ID ADE90646 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1042
ID ADE91793 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1043
ID ADG11685 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US200322655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1044
ID ADG02372 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1045
ID ADG22158 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1046
ID ADG20228 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1047
ID ADF98134 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1048
ID ADG24351 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1049
ID ADF98705 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1050
ID ADG03536 standard; protein; 293 AA.
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DE Human PRO polypeptide #228.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1051
ID ADP99257 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1052
ID ADG16842 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1053
ID ADG05301 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1054
ID ADG19568 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1055
ID ADG13405 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1056
ID ADG08462 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1057
ID ADG15632 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1058
ID ADP97030 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1059
ID ADG06215 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1060
ID ADG23799 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1061
ID ADG04088 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1062
ID ADG24989 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1063
ID ADG07286 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1064
ID ADG07838 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1065
ID ADG55333 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1066
ID ADG60997 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1067
ID ADG62101 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1068
ID ADG82302 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207358-A1.

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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1069
ID ADG57541 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1070
ID ADG56989 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1071
ID ADG55885 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1072
ID ADG56645 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1073
ID ADG71011 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1074
ID ADG58093 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1075
ID ADG53677 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1076
ID ADG71563 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1077
ID ADG81750 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1078
ID ADH19555 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1079
ID ADH30712 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1080
ID ADH12079 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1081
ID ADG52501 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1082
ID ADG54229 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1083
ID ADG81198 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1084
ID ADG56437 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1085
ID ADH12703 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1086
ID ADH21048 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
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RESULT 1087
ID ADG61549 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1088
ID ADH2008 standard; protein: 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1089
ID ADH28636 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1090
ID ADG54781 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1091
ID ADG59821 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1092
ID ADI81245 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1093
ID ADG0988 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1094
ID ADI15459 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1095
ID ADG09336 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1096
ID ADI14791 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1097
ID ADI18386 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1098
ID ADG63667 standard; protein: 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1099
ID ADJ77562 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1100
ID ADI65684 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1101
ID ADM27820 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1102
ID ADK52481 standard; protein: 293 AA.
DE Human kallikrein 5 protein.
PN WO2004021008-A2.
PD 11-MAR-2004.
PA (MOUN ) MOUNT SINAI HOSPITAL.
PA (YOUS/) YOUSEF G.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1103
ID ADM42544 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1104
ID ADM28406 standard; protein: 293 AA.
DE Human PRO polypeptide #228.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1105
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ID AD195888 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1106
ID AD196440 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1107
ID ADR72621 standard; protein; 293 AA.
DE Human renal cell carcinoma-related kallikrein 5 (hK5) protein.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1108
ID ADR72873 standard; protein; 293 AA.
DE Human ovarian cancer-related tumour marker kallikrein 5 (hK5) protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1109
ID AAY14072 standard; protein; 322 AA.
DE Human BS247 specific epitope.
PN WO9922027-A1.
PD 06-MAY-1999.
PA (ABBO) ABBOTT LAB.
Query Match 41.1%; Score 564.5; DB 2; Length 322;
Best Local Similarity 45.3%; Pred. No. 1.6e-35;
RESULT 1110
ID AAM07620 standard; protein; 276 AA.
DE Human NES1 polypeptide.
PN WO9639175-A1.
PD 12-DEC-1996.
PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
Query Match 41.0%; Score 564; DB 2; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1111
ID AAB21327 standard; protein; 276 AA.
DE Human NES1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.0%; Score 564; DB 3; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1112
ID ABG96356 standard; protein; 276 AA.
DE Human ovarian cancer marker OV32.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.0%; Score 564; DB 5; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1113
ID AAU82729 standard; protein; 276 AA.
DE Amino acid sequence of novel human protease #28.
PN WO2000200860-A2.
PD 03-JAN-2002.
PA (SUGR-) SUGEN INC.
Query Match 41.0%; Score 564; DB 5; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1114
ID ADB80527 standard; protein; 276 AA.

DE Ovarian cancer-associated protein #46.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 41.0%; Score 564; DB 7; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1115
ID ADE40473 standard; protein; 276 AA.
DE Human kallikrein 10 (gene ID 2045) protein.
PN WO2003070883-A2.
PD 28-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.0%; Score 564; DB 7; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1116
ID ADN39880 standard; protein; 276 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C250.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 41.0%; Score 564; DB 7; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1117
ID ADN04446 standard; protein; 276 AA.
DE Antipodiatric protein sequence #416.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 41.0%; Score 564; DB 8; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1118
ID ADO89070 standard; protein; 276 AA.
DE Human urological disorder related protein 2045 SEQ.22.
PN WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.0%; Score 564; DB 8; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1119
ID ADR72628 standard; protein; 276 AA.
DE Human renal cell carcinoma-related kallikrein 10 (hK10) protein.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.0%; Score 564; DB 8; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1120
ID ADR72886 standard; protein; 276 AA.
DE Human ovarian cancer-related tumour marker kallikrein 10 (hK10) protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.0%; Score 564; DB 8; Length 276;
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1121
ID AAB21305 standard; protein; 237 AA.
DE Human KLK-L6 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.9%; Score 562; DB 3; Length 237;
Best Local Similarity 48.1%; Pred. No. 1.9e-35;
RESULT 1122
ID AAB21299 standard; protein; 256 AA.
DE Human KLK-L4 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.9%; Score 561.5; DB 3; Length 256;
Best Local Similarity 49.1%; Pred. No. 2.2e-35;
RESULT 1123
ID AAB21309 standard; protein; 287 AA.

PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.9%; Score 561.5; DB 3; Length 287;
Best Local Similarity 46.1%; Pred. No. 2.5e-35;
RESULT 1124
ID ABB98259 standard; protein; 228 AA.
DE Synthetic shortened trypsinogen SEQ ID NO 23.
PN WO200261064-A2.
PD 08-AUG-2002.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
Query Match 40.8%; Score 561; DB 5; Length 228;
Best Local Similarity 46.7%; Pred. No. 2.1e-35;
RESULT 1125
ID AAB21310 standard; protein; 239 AA.
DE Human zyme.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 3; Length 239;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1126
ID AAR44532 standard; protein; 244 AA.
DE Zyme APP-cleaving protease.
PN EP576152-A1.
PD 29-DEC-1993.
PA (ELIL) LILLY & CO ELI.
Query Match 40.8%; Score 561; DB 2; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1127
ID AAM22985 standard; protein; 244 AA.
DE Human serine protease 59 (SP59).
PN JP09149790-A.
PD 10-JUN-1997.
PA (SUNR) SUNTORY LTD.
Query Match 40.8%; Score 561; DB 2; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1128
ID AAW51006 standard; protein; 244 AA.
DE Protease M, a novel serine protease.
PN WO9811238-A2.
PD 19-MAR-1998.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 40.8%; Score 561; DB 2; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1129
ID AAB21323 standard; protein; 244 AA.
DE Human zyme.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 3; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1130
ID AAE37572 standard; protein; 244 AA.
DE Human 2047 protein.
PN WO2003037258-A2.
PD 08-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 40.8%; Score 561; DB 6; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1131
ID ADB80567 standard; protein; 244 AA.
DE Ovarian cancer-associated protein #66.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 40.8%; Score 561; DB 7; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1132
ID ADJ39212 standard; protein; 244 AA.
DE Cancer/angiogenesis/fibroblast-related polypeptide, SEQ ID NO:530.

PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 40.8%; Score 561; DB 7; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1133
ID ADN04074 standard; protein; 244 AA.
DE Antipeptidic protein sequence #232.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1134
ID ADN29289 standard; protein; 244 AA.
DE Human kallikrein 6 associated protein.
PN US2004097452-A1.
PD 20-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1135
ID ADQ89076 standard; protein; 244 AA.
DE Human urological disorder related protein 2047 SEQ:28.
PN WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1136
ID ADR72624 standard; protein; 244 AA.
DE Human renal cell carcinoma-related kallikrein 6 (hk6) protein.
PN WO2004077060-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1137
ID ADR72876 standard; protein; 244 AA.
DE Human ovarian cancer-related tumor marker kallikrein 6 (hk6) protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 8; Length 244;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1138
ID ABG96357 standard; protein; 244 AA.
DE Human ovarian cancer marker OV33.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 40.8%; Score 560; DB 5; Length 244;
Best Local Similarity 46.9%; Pred. No. 2.7e-35;
RESULT 1139
ID AAB21297 standard; protein; 296 AA.
DE Human KIX-L3 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.5%; Score 557; DB 3; Length 296;
Best Local Similarity 46.1%; Pred. No. 5.7e-35;
RESULT 1140
ID AAR67868 standard; protein; 253 AA.
DE Human stratum corneum chymotryptic recombinant enzyme (SCCE).
PN WO9500651-A1.
PD 05-JAN-1995.
PA (SYMB-) SYMBICOM AB.
Query Match 40.4%; Score 555; DB 2; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1141
ID AAW05383 standard; protein; 253 AA.
DE Human amyloid precursor protein protease.
PN WO9631122-A1.

PD 10-OCT-1996.
PA (BLIL) LILLY & CO ELI.
Query Match 40.4%; Score 555; DB 2; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1142
ID ABB84421 standard; peptide; 253 AA.
DE Human SCCE protein N-terminal fragment SEQ ID 48.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
Query Match 40.4%; Score 555; DB 5; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1143
ID ABB84406 standard; protein; 253 AA.
DE Human SCCE protein.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
Query Match 40.4%; Score 555; DB 5; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1144
ID AAU82740 standard; protein; 253 AA.
DE Amino acid sequence of novel human protease #39.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGR-) SUGEN INC.
Query Match 40.4%; Score 555; DB 5; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1145
ID ABU07440 standard; protein; 253 AA.
DE Protein differentially regulated in prostate cancer #43.
PN WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 40.4%; Score 555; DB 6; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1146
ID ABU07471 standard; protein; 253 AA.
DE Protein differentially regulated in prostate cancer #74.
PN WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 40.4%; Score 555; DB 6; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1147
ID ABR58471 standard; protein; 253 AA.
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
PN WO2003029468-A1.
PD 10-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 40.4%; Score 555; DB 6; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1148
ID ADB80484 standard; protein; 253 AA.
DE Ovarian cancer-associated protein #24.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 40.4%; Score 555; DB 7; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1149
ID ADJ68833 standard; protein; 253 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID639.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 40.4%; Score 555; DB 7; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1150
ID ADN39180 standard; protein; 253 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 40.4%; Score 555; DB 7; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1151
ID ADL06515 standard; protein; 253 AA.
DE Human tumour-associated antigenic target (TAT) polypeptide #14.
PN WO2004016225-A2.
PD 26-FEB-2004.
PA (GENTH-) GENTENTECH INC.
Query Match 40.4%; Score 555; DB 8; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1152
ID ADN04182 standard; protein; 253 AA.
DE Antipsoriatic protein sequence #286.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GENTH-) GENTENTECH INC.
Query Match 40.4%; Score 555; DB 8; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1153
ID ADR72880 standard; protein; 253 AA.
DE Human ovarian cancer-related tumour marker kallikrein 7 (HK7) protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN-) MOUNT SINAI HOSPITAL.
Query Match 40.4%; Score 555; DB 8; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1154
ID ADA05734 standard; protein; 252 AA.
DE Human NOV18P protein SEQ ID NO:94.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 40.3%; Score 553.5; DB 6; Length 252;
Best Local Similarity 46.6%; Pred. No. 9e-35;
RESULT 1155
ID ADN62898 standard; protein; 252 AA.
DE Human NOV18P.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUTU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATR/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (BILE/) ELLERMAN K.
PA (MALI/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERRUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (UTWU/) UT W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEB/) AGEES M L.
PA (BERG/) BERGHS C.
PA (DIPV/) DIPPIO V A.

PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 40.3%; Score 553.5; DB 8; Length 252;
Best Local Similarity 46.6%; Pred. No. 9e-35;
RESULT 1156
ID AAY08025 standard; protein; 253 AA.
DE Mouse protease-related protein (PVP).
PN DE19736198-C1.
PD 24-DEC-1998.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
Query Match 40.3%; Score 553.5; DB 2; Length 253;
Best Local Similarity 43.5%; Pred. No. 9e-35;
RESULT 1157
ID ADN62896 standard; protein; 250 AA.
DE Human NOVI18a.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLER I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATY/) PATTRAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENNA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIRI/) DIRIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 40.2%; Score 553; DB 8; Length 250;
Best Local Similarity 44.8%; Pred. No. 9.8e-35;
RESULT 1158
ID AAT77494 standard; protein; 229 AA.
DE Bovine trypsinogen.
PN WO200005384-A1.
PD 03-FEB-2000.
PA (PROD-) PRODIGENE INC.
Query Match 40.2%; Score 552; DB 3; Length 229;
Best Local Similarity 46.3%; Pred. No. 1.1e-34;
RESULT 1159
ID AAR53638 standard; protein; 230 AA.
DE Bovine trypsinogen.
PN EP597681-A1.
PD 18-MAY-1994.
PA (EULI/) LILLY & CO ELI.
Query Match 40.2%; Score 552; DB 2; Length 230;
Best Local Similarity 47.5%; Pred. No. 1.1e-34;
RESULT 1160
ID AAY91926 standard; protein; 231 AA.

DE Recombinant trypsin.
PN WO200017332-A1.
PD 30-MAR-2000.
PA (EULI/) LILLY & CO ELI.
Query Match 40.2%; Score 552; DB 3; Length 231;
Best Local Similarity 46.3%; Pred. No. 1.1e-34;
RESULT 1161
ID AAB80953 standard; protein; 231 AA.
DE Bovine met-phe-trypsinogen.
PN WO20011970-A2.
PD 22-MAR-2001.
PA (EULI/) LILLY & CO ELI.
Query Match 40.2%; Score 552; DB 4; Length 231;
Best Local Similarity 46.3%; Pred. No. 1.1e-34;
RESULT 1162
ID ADA05732 standard; protein; 250 AA.
DE Human NOVI18a protein SEQ ID NO:92.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 40.2%; Score 552; DB 6; Length 250;
Best Local Similarity 44.8%; Pred. No. 1.2e-34;
RESULT 1163
ID ABB84420 standard; peptide; 249 AA.
DE Porcine SCCB protein N-terminal fragment SEQ ID 47.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGBL/) EGBELRUD T.
PA (HANS/) HANSSON L.
Query Match 40.1%; Score 550.5; DB 5; Length 249;
Best Local Similarity 46.7%; Pred. No. 1.5e-34;
RESULT 1164
ID AAB35701 standard; protein; 247 AA.
DE Human trypsin hL amino acid sequence.
PN JP2000253887-A.
PD 19-SEP-2000.
PA (TTPH-) TP PHARMA KK.
Query Match 40.0%; Score 549.5; DB 3; Length 247;
Best Local Similarity 44.0%; Pred. No. 1.8e-34;
RESULT 1165
ID AAU86677 standard; protein; 247 AA.
DE Novel human connective tissue related polypeptide #243.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 4; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1166
ID AAU23752 standard; protein; 247 AA.
DE Novel human enzyme polypeptide #838.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 4; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1167
ID AAU17043 standard; protein; 247 AA.
DE Human novel secreted protein, SEQ ID 284.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 4; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1168
ID ADB60011 standard; protein; 247 AA.
DE Connective tissue antigen (CTA) #243.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 7; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1169
ID AAW81767 standard; peptide; 223 AA.

DE Bovine TRYP peptide fragment.
PN JP10287696-A.
PD 27-OCT-1998.
PA (YAK-) YAKU BUNSHI SEKKEI KENKUTSUO KK.
Query Match 39.8%; Score 547; DB 2; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1170
ID AAY69973 standard; protein; 223 AA.
DE TRYP protein.
PN WO9962004-A1.
PD 02-DEC-1999.
PA (MEDT-) INST MEDICINAL MOLECULAR DESIGN INC.
Query Match 39.8%; Score 547; DB 3; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1171
ID ABG31841 standard; protein; 223 AA.
DE Example protein #3 used in three-dimensional structure analysis method.
PN WO200257854-A1.
PD 25-JUL-2002.
PA (MITU-) MITSUBISHI CHEM CORP.
Query Match 39.8%; Score 547; DB 5; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1172
ID ADC73287 standard; protein; 223 AA.
DE Bovine 2PTC_E protein - SEQ ID 13.
PN WO2003060765-A1.
PD 24-JUL-2003.
PA (AJIN-) AJINOMOTO CO INC.
Query Match 39.8%; Score 547; DB 7; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1173
ID ADD35545 standard; protein; 223 AA.
DE Cationic bovine trypsinogen TRY1.
PN WO2003040093-A2.
PD 15-MAY-2003.
PA (FARB-) BAYER AG.
Query Match 39.8%; Score 547; DB 7; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1174
ID AAR53637 standard; protein; 224 AA.
DE Bovine trypsin.
PN EP597681-A1.
PD 18-MAY-1994.
PA (ELIL-) LILLY & CO ELI.
Query Match 39.8%; Score 547; DB 2; Length 224;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
RESULT 1175
ID AAY91925 standard; protein; 233 AA.
DE Trypsinogen analogue.
PN WO200017332-A1.
PD 30-MAR-2000.
PA (ELIL-) LILLY & CO ELI.
Query Match 39.8%; Score 547; DB 3; Length 233;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1176
ID ADI39734 standard; protein; 244 AA.
DE Human protease M (prom) protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCT.
Query Match 39.7%; Score 546; DB 8; Length 244;
Best Local Similarity 45.8%; Pred. No. 3.3e-34;
RESULT 1177
ID ADI37158 standard; protein; 244 AA.
DE Human protease m (Prom).
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Query Match 39.7%; Score 546; DB 8; Length 244;
Best Local Similarity 45.8%; Pred. No. 3.3e-34;
RESULT 1178

ID AAY78974 standard; protein; 247 AA.
DE Canine cationic trypsinogen amino acid sequence.
PN WO200009739-A1.
PD 24-FEB-2000.
PA (FUJY-) FUJI YAKUHIN KOGYO KK.
Query Match 39.7%; Score 546; DB 3; Length 247;
Best Local Similarity 45.6%; Pred. No. 3.3e-34;
RESULT 1179
ID ADA05742 standard; protein; 247 AA.
DE Human NOVI18f protein SEQ ID NO:102.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.7%; Score 546; DB 6; Length 247;
Best Local Similarity 45.5%; Pred. No. 3.3e-34;
RESULT 1180
ID ADN62906 standard; protein; 247 AA.
DE Human NOVI18f.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT-) SMITHSON G.
PA (MILL-) MILLET I.
PA (PEYM-) PEYMAN J A.
PA (KEKU-) KERUDA R.
PA (JUUJ-) JU J.
PA (LILL-) LI L.
PA (GUOX-) GUO X.
PA (PATY-) PATTURAJAN M.
PA (SPYT-) SPYTEK K A.
PA (EDIN-) EDINGER S R.
PA (ELLE-) ELLERMAN K.
PA (MALY-) MALYANKAR U M.
PA (ORTT-) ORT T.
PA (GORM-) GORMAN L.
PA (ZERR-) ZERRHUSSEN B D.
PA (ANDE-) ANDERSON D W.
PA (ZHON-) ZHONG M.
PA (CATT-) CATTERTON E.
PA (JIMW-) JI W.
PA (MILL-) MILLER C E.
PA (RAST-) RASTELTI L.
PA (STON-) STONE D J.
PA (PENA-) PENNA C E A.
PA (SHEN-) SHENOY S G.
PA (SHIM-) SHIMKETS R A.
PA (ROTH-) ROTHENBERG M E.
PA (LEAC-) LEACH M D.
PA (AGEE-) AGEE M L.
PA (BERG-) BERGHS C.
PA (DIPJ-) DIPIPPO V A.
PA (EISE-) EISEN A.
PA (GANG-) GANGOLI E A.
PA (RIRG-) RIRGER D K.
PA (SPAD-) SPADERNA S K.
Query Match 39.7%; Score 546; DB 8; Length 247;
Best Local Similarity 45.5%; Pred. No. 3.3e-34;
RESULT 1181
ID AAB98502 standard; protein; 225 AA.
DE Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
PN WO200128056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 39.7%; Score 545; DB 4; Length 225;
Best Local Similarity 46.5%; Pred. No. 3.6e-34;
RESULT 1182
ID AAY78975 standard; protein; 246 AA.
DE Canine anionic trypsinogen amino acid sequence.
PN WO200009739-A1.
PD 24-FEB-2000.
PA (FUJY-) FUJI YAKUHIN KOGYO KK.
Query Match 39.7%; Score 545; DB 3; Length 246;
Best Local Similarity 44.2%; Pred. No. 4e-34;
RESULT 1183

ID AAB21326 standard; protein; 257 AA.
DE Human HSCE.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 39.6%; Score 544; DB 3; Length 257;
Best Local Similarity 44.1%; Pred. No. 5e-34;
RESULT 1184
ID AAM64260 standard; protein; 246 AA.
DE Human amyloid beta-protein precursor inhibitor.
PN WO9824886-A1.
PD 11-JUN-1998.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 39.5%; Score 543; DB 2; Length 246;
Best Local Similarity 44.5%; Pred. No. 5.7e-34;
RESULT 1185
ID ADC73299 standard; protein; 220 AA.
DE Stereosestructure-related 2PTC protein.
PN WO2003060765-A1.
PD 24-JUL-2003.
PA (AJIN) AJINOMOTO CO INC.
PA (UMEV) UMEYAMA H.
Query Match 39.4%; Score 541; DB 7; Length 220;
Best Local Similarity 46.8%; Pred. No. 7.2e-34;
RESULT 1186
ID ADC73301 standard; protein; 279 AA.
DE Stereosestructure-related 2PTC protein.
PN WO2003060765-A1.
PD 24-JUL-2003.
PA (AJIN) AJINOMOTO CO INC.
PA (UMEV) UMEYAMA H.
Query Match 39.4%; Score 541; DB 7; Length 279;
Best Local Similarity 46.8%; Pred. No. 9.2e-34;
RESULT 1187
ID AD116686 standard; protein; 259 AA.
DE Human NOVX protein to treat human pathological conditions SeqID222.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 39.3%; Score 539.5; DB 5; Length 259;
Best Local Similarity 44.4%; Pred. No. 1.1e-33;
RESULT 1188
ID ADN42340 standard; protein; 259 AA.
DE Human novel proteinNOV 62.
PD 19-FEB-2004.
PA (TCHE) TCHERNEV V T.
PA (SPYT) SPYTEK K A.
PA (ZERH) ZERHUSEN B D.
PA (PATU) PATTURAJAN M.
PA (SHIM) SHIMKETS R A.
PA (LILU) LI L.
PA (GANG) GANGOLLI E A.
PA (PADI) PADIGARU M.
PA (ANDE) ANDERSON D W.
PA (RAST) RASTELLI L.
PA (MILL) MILLER C E.
PA (GERL) GERLACH V.
PA (TAUP) TAUPFER R J.
PA (GUSE) GUSEV V Y.
PA (COLM) COLMAN S D.
PA (WOLE) WOLENC A R.
PA (PENNA) PENNA C E A.
PA (FURT) FORTAK K.
PA (GROS) GROSSE W M.
PA (ALSO) ALSOBROOK J P.
PA (LEPL) LEPLAY D M.
PA (RIEG) RIEGER D K.
PA (BURG) BURGESS C E.
Query Match 39.3%; Score 539.5; DB 8; Length 259;
Best Local Similarity 44.4%; Pred. No. 1.1e-33;
RESULT 1189
ID ABB78122 standard; peptide; 223 AA.

DE Amino acid sequence of trypsin.
PN US2002072863-A1.
PD 13-JUN-2002.
PA (FUUT) FUJITSU LTD.
Query Match 39.2%; Score 538; DB 5; Length 223;
Best Local Similarity 45.6%; Pred. No. 1.2e-33;
RESULT 1190
ID ABB83322 standard; protein; 223 AA.
DE Partial trypsin sequence.
PN US2002035434-A1.
PD 21-MAR-2002.
PA (FUUT) FUJITSU LTD.
Query Match 39.2%; Score 538; DB 5; Length 223;
Best Local Similarity 45.6%; Pred. No. 1.2e-33;
RESULT 1191
ID ABB84419 standard; peptide; 243 AA.
DE Bovine SCCE protein N-terminal fragment SEQ ID 46.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL) EGELRUD T.
PA (HANS) HANSSON L.
Query Match 38.7%; Score 531.5; DB 5; Length 243;
Best Local Similarity 43.8%; Pred. No. 4.3e-33;
RESULT 1192
ID ABB04644 standard; protein; 240 AA.
DE Engraulis japonicus trypsinogen (atry I) SEQ ID NO:1.
PN JP2001269173-A.
PD 02-OCT-2001.
PA (NISB) JAPAN TOBACCO INC.
Query Match 38.2%; Score 525; DB 5; Length 240;
Best Local Similarity 45.7%; Pred. No. 1.3e-32;
RESULT 1193
ID AAM64261 standard; protein; 232 AA.
DE Kallikrein substrate binding site.
PN WO9824886-A1.
PD 11-JUN-1998.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 38.1%; Score 524; DB 2; Length 232;
Best Local Similarity 43.6%; Pred. No. 1.6e-32;
RESULT 1194
ID ABB84423 standard; peptide; 249 AA.
DE Murine SCCE protein N-terminal fragment SEQ ID 50.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL) EGELRUD T.
PA (HANS) HANSSON L.
Query Match 38.0%; Score 521.5; DB 5; Length 249;
Best Local Similarity 43.0%; Pred. No. 2.6e-32;
RESULT 1195
ID ABR96164 standard; protein; 261 AA.
DE Human NOV13a protein SEQ ID NO:70.
PN WO200290568-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 37.8%; Score 519.5; DB 6; Length 261;
Best Local Similarity 40.0%; Pred. No. 3.9e-32;
RESULT 1196
ID AD115205 standard; protein; 232 AA.
DE Pancreatic kallikrein #1.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL, SHENZHEN CITY.
Query Match 37.8%; Score 519; DB 7; Length 232;
Best Local Similarity 44.5%; Pred. No. 3.8e-32;
RESULT 1197
ID ABB70276 standard; protein; 247 AA.
DE Human Serine Protease TLSP-like protein.
PN WO200255702-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 37.6%; Score 516; DB 5; Length 247;
Best Local Similarity 42.5%; Pred. No. 6.9e-32;
RESULT 1198

ID AAW94493 standard; protein; 268 AA.
DE Human kallikrein.
PN WO9842849-A1.
PD 01-OCT-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 37.4%; Score 514; DB 2; Length 268;
Best Local Similarity 46.4%; Pred. No. 1.1e-31;
RESULT 1199
ID ABB04645 standard; protein; 241 AA.
DE Emgraulis japonicus trypsinogen (atry I) SEQ ID NO.2.
PN JP200126173-A.
PD 02-OCT-2001.
PA (NISR-) JAPAN TOBACCO INC.
Query Match 36.7%; Score 504; DB 5; Length 241;
Best Local Similarity 45.9%; Pred. No. 5.6e-31;
RESULT 1200
ID AAU87693 standard; protein; 247 AA.
DE Human pancreatic tumour protein #5.
PN WO200212331-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 36.5%; Score 501; DB 5; Length 247;
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1201
ID ADN04140 standard; protein; 247 AA.
DE Antiproteolytic protein sequence #265.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 36.5%; Score 501; DB 8; Length 247;
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1202
ID ADN99594 standard; protein; 247 AA.
DE Novel human protein sequence #410.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 36.5%; Score 501; DB 8; Length 247;
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1203
ID ADQ30589 standard; protein; 247 AA.
DE Pancreas cancer marker - trypsin II precursor.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOPE-) HOFFMANN LA ROCHE & CO AG F.
Query Match 36.5%; Score 501; DB 8; Length 247;
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1204
ID ABR41530 standard; protein; 261 AA.
DE Human DITRP protein modification/maintenance protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 36.5%; Score 501; DB 6; Length 261;
Best Local Similarity 43.3%; Pred. No. 1e-30;
RESULT 1205
ID AAB03862 standard; protein; 223 AA.
DE Human neurosin amino acid sequence.
PN WO2000031284-A1.
PD 02-JUN-2000.
PA (FUZO-) FUZO PHARM IND LTD.
Query Match 36.4%; Score 500; DB 3; Length 223;
Best Local Similarity 43.5%; Pred. No. 1.1e-30;
RESULT 1206
ID AAB21294 standard; protein; 254 AA.
DE Human Kik-Ii protein #2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN-) MOUNT SINAI HOSPITAL.
Query Match 36.2%; Score 498; DB 3; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1207

ID AAM01174 standard; protein; 254 AA.
DE Human prostate-specific amino acid sequence P703P.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 4; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1208
ID AAU69819 standard; protein; 254 AA.
DE Human prostate cDNA encoded protein #27.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 4; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1209
ID AAG39059 standard; protein; 254 AA.
DE Human prostate-specific amino acid of P703P.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 4; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1210
ID ABU71710 standard; protein; 254 AA.
DE Prostate cancer specific antigen P703P #7.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJU/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIANG/) JIANG Y.
PA (KALOS/) KALOS M D.
PA (FRANG/) FRANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUN/) HOUNGTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match 36.2%; Score 498; DB 4; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1211
ID ABB95279 standard; protein; 254 AA.
DE Human P703P putative full length protein SEQ ID NO 525.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUJU/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIANG/) JIANG Y.
PA (KALOS/) KALOS M D.
PA (FRANG/) FRANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.

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PA (HEND/) HENDERSON R A.
Query Match 36.2%; Score 498; DB 5; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1212
ID ABP54360 standard; protein; 254 AA.
DE Human KLK4 protein SEQ ID NO:13.
PN WO200277243-A1.
PD 03-OCT-2002.
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
Query Match 36.2%; Score 498; DB 6; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1213
ID ABP54357 standard; protein; 254 AA.
DE Human KLK4 protein SEQ ID NO:6.
PN WO200277243-A1.
PD 03-OCT-2002.
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
Query Match 36.2%; Score 498; DB 6; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1214
ID ABP54391 standard; protein; 254 AA.
DE Prostate tumour specific protein sequence SEQ ID 525.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 6; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1215
ID ADB13975 standard; protein; 254 AA.
DE Human prostate specific protein P703P.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 7; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1216
ID ADG26391 standard; protein; 254 AA.
DE Human prostate-specific polypeptide #60.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 7; Length 254;
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1217
ID AAB74830 standard; protein; 1079 AA.
DE Prostate tumour antigen amino acid sequence for a fusion protein.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.2%; Score 498; DB 4; Length 1079;
Best Local Similarity 43.1%; Pred. No. 7.6e-30;
RESULT 1218
ID ABU71860 standard; protein; 1079 AA.
DE Prostate specific antigen fusion protein #2.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUUT/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (PANG/) PANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.

PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUN/) HOUNGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match 36.2%; Score 498; DB 4; Length 1079;
Best Local Similarity 43.1%; Pred. No. 7.6e-30;
RESULT 1219
ID AD117268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOX domain SegID 804.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 36.2%; Score 497.5; DB 5; Length 230;
Best Local Similarity 47.4%; Pred. No. 1.7e-30;
RESULT 1220
ID AD117276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOX domain SegID 812.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 36.2%; Score 497.5; DB 5; Length 230;
Best Local Similarity 47.4%; Pred. No. 1.7e-30;
RESULT 1221
ID ADJ83075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZBRH/) ZERHUSEN B D.
PA (PART/) PARTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASHMAN S J.
PA (BOLD/) BOLDIG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER B.
PA (MILL/) MILLER J.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 36.2%; Score 497.5; DB 7; Length 230;
Best Local Similarity 47.4%; Pred. No. 1.7e-30;
RESULT 1222
ID ADJ27345 standard; peptide; 280 AA.
DE Amino acid sequence of trypsinogen.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFEY/) AFEYAN N B.
Query Match 36.2%; Score 497.5; DB 8; Length 280;
Best Local Similarity 42.7%; Pred. No. 2.1e-30;
RESULT 1223
ID ADJ27346 standard; peptide; 461 AA.
DE Amino acid sequence of trypsinogen-0aa-eps5.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFEY/) AFEYAN N B.
Query Match 36.2%; Score 497.5; DB 8; Length 461;
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Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1224
ID ADI27347 standard; peptide; 464 AA.
DE Amino acid sequence of trypsinogen-3aa-eps5.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFEPY/) APEYAN N B.
Query Match
Best Local Similarity 36.2%; Score 497.5; DB 8; Length 464;
RESULT 1225
ID ADI27348 standard; peptide; 485 AA.
DE Amino acid sequence of trypsinogen-20aa-sp55.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFEPY/) APEYAN N B.
Query Match
Best Local Similarity 42.7%; Pred. No. 3.5e-30;
RESULT 1226
ID AAB21307 standard; protein; 249 AA.
DE Human prostatic.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 36.2%; Score 497.5; DB 3; Length 249;
RESULT 1227
ID AAB21320 standard; protein; 254 AA.
DE Human prostatic.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 36.2%; Score 497; DB 3; Length 254;
RESULT 1228
ID AAY7525 standard; protein; 254 AA.
DE Human prostatic antigen #3.
PN WO200104143-A2.
PD 18-JUN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 36.2%; Score 497; DB 4; Length 254;
RESULT 1229
ID AAY74901 standard; protein; 254 AA.
DE Protein sequence of prostate homologue #3.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 36.2%; Score 497; DB 5; Length 254;
RESULT 1230
ID AAY74932 standard; protein; 254 AA.
DE Amino acid sequence of prostate protein fragment #3.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 36.2%; Score 497; DB 5; Length 254;
RESULT 1231
ID AAW60592 standard; protein; 248 AA.
DE Human prostate-specific kallikrein (HPSK) protein.
PN WO9820117-A1.
PD 14-MAY-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity 36.1%; Score 496.5; DB 2; Length 248;
RESULT 1232
ID AAY72524 standard; protein; 248 AA.
DE Human prostatic antigen #2.
PN WO200104143-A2.
PD 18-JUN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 40.4%; Pred. No. 3e-30;
LENGTH 262;
RESULT 1236
ID ADR90673 standard; protein; 246 AA.
DE Human trypsinogen partial protein.
PN WO2004078777-A2.
PD 16-SEP-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match
Best Local Similarity 36.0%; Score 494.5; DB 8; Length 246;
RESULT 1237
ID AAB21321 standard; protein; 247 AA.
DE Human trypsinogen.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 41.9%; Pred. No. 3.1e-30;
LENGTH 247;
RESULT 1238
ID ABR54239 standard; protein; 247 AA.
DE Human NOV35a protein SEQ ID NO:146.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 36.0%; Score 494.5; DB 6; Length 247;
RESULT 1239
ID ABR54241 standard; protein; 247 AA.
DE Human NOV35c protein SEQ ID NO:150.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 41.9%; Pred. No. 3.1e-30;
LENGTH 247;
RESULT 1240
ID ADQ30588 standard; protein; 247 AA.
DE Pancreas cancer marker - trypsin I precursor.
PN WO200405519-A2.
PD 01-JUL-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match
Best Local Similarity 36.0%; Score 494.5; DB 8; Length 247;
RESULT 1241
ID AAM01173 standard; protein; 254 AA.


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DE Human prostate-specific amino acid mature form of P703P.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 36.0%; Score 494; DB 4; Length 254;
PD 04-OCT-2001.
DE Human prostate CDNA encoded protein #26.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 36.0%; Score 494; DB 4; Length 254;
PD 17-MAY-2001.
DE Human prostate-specific mature protein of P703P.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 36.0%; Score 494; DB 4; Length 254;
PD 19-DEC-2002.
DE Prostate cancer associated protein #12.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FRANG/) FRANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNETIL P D.
PA (HOUO/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
Best Local Similarity 36.0%; Score 494; DB 4; Length 254;
PD 21-FEB-2002.
DE Human P703P mature protein SEQ ID NO 523.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FRANG/) FRANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Query Match
Best Local Similarity 36.0%; Score 494; DB 5; Length 262;
PD 15-SEP-2000.
DE Human kallikrein protein.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM/) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUII/) HUI L.
Query Match
Best Local Similarity 36.0%; Score 494; DB 5; Length 262;
PD 11-DEC-2002.
DE Human pancreatic kallikrein.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMT-) REMIN HOSPITAL SHENZHEN CITY.
Query Match
Best Local Similarity 36.0%; Score 494; DB 7; Length 262;
PD 19-FEB-2004.
DE Human kallikrein protein (KLK1).
PN US2004033582-A1.
PD 19-FEB-2004.
PA (EDMO/) EDMONDS M.
PA (HUII/) HUI L.
PA (PERR/) PERRONE M.
PA (POWE/) POWELL J R.
PA (RAMA/) RAMANATHAN C S.
PA (SWAN/) SWANSON B.
PA (TSUC/) TSUCHIHASHI Z.
PA (ZERR/) ZERBA K.
Query Match
Best Local Similarity 36.0%; Score 494; DB 8; Length 262;
PD 15-JUL-2004.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1317.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
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Query Match 36.0%; Score 494; DB 8; Length 262;
 Best Local Similarity 40.4%; Pred. No. 3.6e-30;
 RESULT 1254
 ID AD834891 standard; protein; 262 AA.
 DE Human autoimmune disease-related protein - SEQ ID NO:105.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 36.0%; Score 494; DB 8; Length 262;
 Best Local Similarity 40.4%; Pred. No. 3.6e-30;
 RESULT 1255
 ID ABR54277 standard; protein; 240 AA.
 DE Human trypsinogen protein SEQ ID NO:341.
 PN WO2003023001-A2.
 PD 20-MAR-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 35.9%; Score 493.5; DB 6; Length 240;
 Best Local Similarity 42.6%; Pred. No. 3.6e-30;
 RESULT 1256
 ID AAB21316 standard; protein; 241 AA.
 DE Human trypsinogen.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Query Match 35.9%; Score 493.5; DB 3; Length 241;
 Best Local Similarity 42.6%; Pred. No. 3.6e-30;
 RESULT 1257
 ID ADN04297 standard; protein; 247 AA.
 DE Antiprosclerotic protein sequence #343.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 35.9%; Score 493; DB 8; Length 247;
 Best Local Similarity 42.1%; Pred. No. 4.1e-30;
 RESULT 1258
 ID AAB21308 standard; protein; 253 AA.
 DE Human EMSP.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Query Match 35.9%; Score 493; DB 3; Length 253;
 Best Local Similarity 42.8%; Pred. No. 4.2e-30;
 RESULT 1259
 ID AAB21324 standard; protein; 258 AA.
 DE Human EMSP.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Query Match 35.9%; Score 493; DB 3; Length 258;
 Best Local Similarity 42.8%; Pred. No. 4.2e-30;
 RESULT 1260
 ID AAW71005 standard; protein; 262 AA.
 DE Human prostate-associated kallikrein designated HPAK.
 PN WO9832265-A1.
 PD 30-JUL-1998.
 PA (INCY-) INCYTE PHARM INC.
 Query Match 35.9%; Score 493; DB 2; Length 262;
 Best Local Similarity 40.4%; Pred. No. 4.3e-30;
 RESULT 1261
 ID ABB74711 standard; protein; 262 AA.
 DE Human glandular kallikrein 1 precursor protein SEQ ID NO:600.
 PN WO200281646-A2.
 PD 17-OCT-2002.
 PA (CTL-) CTL IMMUNOTHERAPIES CORP.
 Query Match 35.9%; Score 493; DB 6; Length 262;
 Best Local Similarity 40.4%; Pred. No. 4.3e-30;
 RESULT 1262
 ID ADL15204 standard; protein; 262 AA.
 DE Pancreatic kallikrein #1.
 PN CN1384199-A.
 PD 11-DEC-2002.
 PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
 Query Match 35.9%; Score 493; DB 7; Length 262;

Best Local Similarity 40.4%; Pred. No. 4.3e-30;
 RESULT 1263
 ID ADM72846 standard; protein; 263 AA.
 DE Human glandular kallikrein 1 protein SEQ ID NO:105.
 PN WO2004022709-A2.
 PD 18-MAR-2004.
 PA (MANN-) MANNKIND CORP.
 Query Match 35.9%; Score 493; DB 8; Length 263;
 Best Local Similarity 40.4%; Pred. No. 4.3e-30;
 RESULT 1264
 ID AAB98503 standard; protein; 225 AA.
 DE Human trypsin serine protease catalytic domain.
 PN WO200129056-A1.
 PD 26-APR-2001.
 PA (UYAR-) UNIV ARKANSAS.
 Query Match 35.8%; Score 492; DB 4; Length 225;
 Best Local Similarity 43.7%; Pred. No. 4.4e-30;
 RESULT 1265
 ID AAW93488 standard; protein; 230 AA.
 DE Human trypsinogen variant protein.
 PN WO9910503-A1.
 PD 04-MAR-1999.
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 Query Match 35.8%; Score 492; DB 2; Length 230;
 Best Local Similarity 43.7%; Pred. No. 4.5e-30;
 RESULT 1266
 ID AAB21315 standard; protein; 256 AA.
 DE Human KLK1.
 PN WO200053776-A2.
 PD 14-SEP-2000.
 PA (MOUN) MOUNT SINAI HOSPITAL.
 Query Match 35.8%; Score 492; DB 3; Length 256;
 Best Local Similarity 41.1%; Pred. No. 5e-30;
 RESULT 1267
 ID AAP95121 standard; protein; 262 AA.
 DE Kallikrein encoded by clone lambda HK65a.
 PN EP297913-A.
 PD 04-JAN-1989.
 PA (AMGE-) AMGEN.
 Query Match 35.8%; Score 492; DB 1; Length 262;
 Best Local Similarity 40.4%; Pred. No. 5.2e-30;
 RESULT 1268
 ID ABG76998 standard; protein; 262 AA.
 DE Human kallikrein protein variant #2.
 PN WO200261131-A2.
 PD 08-AUG-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUII/) HUI L.
 Query Match 35.8%; Score 492; DB 5; Length 262;
 Best Local Similarity 40.4%; Pred. No. 5.2e-30;
 RESULT 1269
 ID AAB54293 standard; protein; 267 AA.
 DE Human pancreatic cancer antigen protein sequence SEQ ID NO:745.
 PN WO200053320-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 35.8%; Score 492; DB 3; Length 267;
 Best Local Similarity 40.4%; Pred. No. 5.3e-30;
 RESULT 1270
 ID ABB77002 standard; protein; 262 AA.
 DE Human kallikrein 1 polymorphic sequence.
 PN WO200261131-A2.
 PD 08-AUG-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUII/) HUI L.
 Query Match 35.7%; Score 491; DB 5; Length 262;
 Best Local Similarity 40.4%; Pred. No. 6.2e-30;
 RESULT 1271
 ID ADA05744 standard; protein; 224 AA.
 DE Human NOV18g protein SEQ ID NO:104.
 PN WO2003029424-A2.

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PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 35.7%; Score 490; DB 6; Length 224;
Best Local Similarity 45.3%; Pred. No. 6.3e-30;
RESULT 1272
ID ADN62908 standard; protein; 224 AA.
DE Human NOV18g.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLER I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERRHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JTWI/) UT W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOV S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEER M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 35.7%; Score 490; DB 8; Length 224;
Best Local Similarity 45.3%; Pred. No. 6.3e-30;
RESULT 1273
ID AAE00397 standard; protein; 234 AA.
DE Human serine protease, PROST 07.
PN WO200125446-A1.
PD 12-APR-2001.
PA (SCHD/) SCHERING AG.
Query Match 35.6%; Score 489.5; DB 4; Length 234;
Best Local Similarity 43.0%; Pred. No. 7.2e-30;
RESULT 1274
ID AAY25510 standard; protein; 231 AA.
DE Human prostate serine protease protein.
PN EP936270-A2.
PD 18-AUG-1999.
PA (BADI/) BASF AG.
Query Match 35.6%; Score 488.5; DB 2; Length 231;
Best Local Similarity 43.9%; Pred. No. 8.4e-30;
RESULT 1275
ID ADN04726 standard; protein; 247 AA.
DE Antiproteolytic protein sequence #544.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH/) GENENTECH INC.
Query Match 35.5%; Score 488; DB 8; Length 247;
Best Local Similarity 42.3%; Pred. No. 9.9e-30;
RESULT 1276
ID ADN95953 standard; protein; 247 AA.
DE Novel human protein sequence #409.
PN WO2004038003-A2.

PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 35.5%; Score 488; DB 8; Length 247;
Best Local Similarity 42.3%; Pred. No. 9.9e-30;
RESULT 1277
ID AAM01227 standard; protein; 449 AA.
DE P703P and PSA fusion amino acid sequence.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 35.5%; Score 487.5; DB 4; Length 449;
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1278
ID AAU69872 standard; protein; 449 AA.
DE Human prostate serum antigen/p703p fusion protein.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 35.5%; Score 487.5; DB 4; Length 449;
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1279
ID ABU7163 standard; protein; 449 AA.
DE Prostate cancer specific antigen fusion protein #1.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIANG/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUN/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match 35.5%; Score 487.5; DB 4; Length 449;
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1280
ID ABB95332 standard; protein; 449 AA.
DE Human P703P/PSA fusion protein SEQ ID NO 617.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIANG/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Query Match 35.5%; Score 487.5; DB 5; Length 449;
Best Local Similarity 44.1%; Pred. No. 2e-29;
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PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 35.3%; Score 484.5; DB 7; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.9e-29;
RESULT 1292
ID AAM83249 standard; protein: 261 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3498.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 35.2%; Score 484; DB 8; Length 261;
Best Local Similarity 43.5%; Pred. No. 2.1e-29;
RESULT 1293
ID AAM83250 standard; protein: 333 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3499.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 35.2%; Score 484; DB 8; Length 333;
Best Local Similarity 43.5%; Pred. No. 2.7e-29;
RESULT 1294
ID AAM57740 standard; protein: 240 AA.
DE Trypsinogen-like protein.
PN JP10099080-A.
PD 21-APR-1998.
PA (SHIS-) SHISEIDO CO LTD.
Query Match 35.2%; Score 483.5; DB 2; Length 240;
Best Local Similarity 42.5%; Pred. No. 2.1e-29;
RESULT 1295
ID ADL15206 standard; protein: 260 AA.
DE Pancreatic kallikrein #2.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 35.2%; Score 483; DB 7; Length 260;
Best Local Similarity 39.8%; Pred. No. 2.5e-29;
RESULT 1296
ID AAB21293 standard; protein: 237 AA.
DE Human KLK-L1 protein #1.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN-) MOUNT SINAI HOSPITAL.
Query Match 35.1%; Score 482.5; DB 3; Length 237;
Best Local Similarity 42.2%; Pred. No. 2.5e-29;
RESULT 1297
ID AAP70568 standard; protein: 262 AA.
DE Human kallikrein-like substance has hypotensive activity.
PN JP62126980-A.
PD 09-JUN-1987.
PA (NAKA-) NAKANISHI S.
Query Match 35.0%; Score 481; DB 1; Length 262;
Best Local Similarity 40.0%; Pred. No. 3.6e-29;
RESULT 1298
ID AAU01290 standard; protein: 216 AA.
DE Human serine protease HETPA37p.
PN WO200123587-A2.
PD 05-APR-2001.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match 34.8%; Score 477.5; DB 4; Length 216;
Best Local Similarity 44.3%; Pred. No. 5.5e-29;
RESULT 1299
ID AAU72526 standard; protein: 226 AA.
DE Human proctase antigen P703PDS sequence.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 4; Length 226;
Best Local Similarity 43.8%; Pred. No. 5.8e-29;
RESULT 1300
ID AAU74902 standard; protein: 226 AA.
DE Protein sequence of proctase homologue #4.
PA (INCY-) INCYTE CORP.

PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 5; Length 226;
Best Local Similarity 43.8%; Pred. No. 5.8e-29;
RESULT 1301
ID AAU74933 standard; protein: 226 AA.
DE Amino acid sequence of proctase protein fragment #4.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 5; Length 226;
Best Local Similarity 43.8%; Pred. No. 5.8e-29;
RESULT 1302
ID AAU72522 standard; protein: 312 AA.
DE NSI-P703P-His fusion protein.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 4; Length 312;
Best Local Similarity 43.8%; Pred. No. 8.1e-29;
RESULT 1303
ID AAU74768 standard; protein: 312 AA.
DE Amino acid sequence of wild-type NSI-P703-His fusion protein.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 5; Length 312;
Best Local Similarity 43.8%; Pred. No. 8.1e-29;
RESULT 1304
ID AAU74929 standard; protein: 312 AA.
DE Amino acid sequence of wild-type NSI-P703P-His fusion protein.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.8%; Score 477.5; DB 5; Length 312;
Best Local Similarity 43.8%; Pred. No. 8.1e-29;
RESULT 1305
ID ABU71886 standard; protein: 344 AA.
DE Human prostate specific antigen (PSA) epitope #26.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ-) XU J.
PA (DILL-) DILLON D C.
PA (MITC-) MITCHAM J L.
PA (HARL-) HARLOCKER S L.
PA (JIAN-) JIANG Y.
PA (KALO-) KALOS M D.
PA (FANG-) FANGER G R.
PA (RETT-) RETTER M W.
PA (STOL-) STOLK J A.
PA (DAYC-) DAY C H.
PA (VEDV-) VEDVICK T S.
PA (CART-) CARTER D.
PA (LISX-) LI S X.
PA (WANG-) WANG A.
PA (SKEI-) SKEIKY Y A W.
PA (HEPL-) HEPLER W T.
PA (HEND-) HENDERSON R A.
PA (HURA-) HURAL J.
PA (MCNE-) MCNEILL P D.
PA (HOUG-) HUGHTON R L.
PA (DBAS-) Y DE BASSOLS C V.
PA (FOYT-) FOY T M.
Query Match 34.8%; Score 477.5; DB 4; Length 344;
Best Local Similarity 43.8%; Pred. No. 8.9e-29;
RESULT 1306
ID AAM82601 standard; protein: 239 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2850.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

Query Match 34.6%; Score 475.5; DB 8; Length 239;
 Best Local Similarity 40.1%; Pred. No. 8.8e-29;
 RESULT 1307
 ID ABM82602 standard; protein; 239 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:2851.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 34.6%; Score 475.5; DB 8; Length 239;
 Best Local Similarity 40.1%; Pred. No. 8.8e-29;
 RESULT 1308
 ID ABM82603 standard; protein; 239 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:2852.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 34.6%; Score 475.5; DB 8; Length 239;
 Best Local Similarity 40.1%; Pred. No. 8.8e-29;
 RESULT 1309
 ID ADN99649 standard; protein; 280 AA.
 DE Novel human protein sequence #465.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 34.4%; Score 473; DB 8; Length 280;
 Best Local Similarity 37.7%; Pred. No. 1.6e-28;
 RESULT 1310
 ID AAY8208 standard; protein; 220 AA.
 DE Human immunogenic prostate tumour protein sequence SEQ ID NO:327.
 PN WO200004149-A2.
 PD 27-JAN-2000.
 PA (CORI-) CORIXA CORP.
 Query Match 34.4%; Score 472.5; DB 3; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1311
 ID AAM01123 standard; protein; 220 AA.
 DE Human prostate-specific amino acid sequence P703PDE6.
 PN WO200151633-A2.
 PD 19-JUL-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 34.4%; Score 472.5; DB 4; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1312
 ID AAU69768 standard; protein; 220 AA.
 DE Human prostate cDNA encoded protein #8.
 PN WO200173032-A2.
 PD 04-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 34.4%; Score 472.5; DB 4; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1313
 ID AAB74806 standard; protein; 220 AA.
 DE Prostate tumour antigen predicted amino acid sequence for P703PDES.
 PN WO200125272-A2.
 PD 12-APR-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 34.4%; Score 472.5; DB 4; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1314
 ID AAG99008 standard; protein; 220 AA.
 DE Human prostate-specific amino acid sequence P703PDES.
 PN WO200134802-A2.
 PD 17-MAY-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 34.4%; Score 472.5; DB 4; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1315
 ID AAG62147 standard; protein; 220 AA.
 DE Human P703P inventive antigen SEQ ID NO: 330.
 PN WO200125273-A2.
 PD 12-APR-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 34.4%; Score 472.5; DB 4; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1320
 ID ADG36193 standard; protein; 220 AA.
 DE Human prostate-specific polypeptide #9.

Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1316
 ID ABU71659 standard; protein; 220 AA.
 DE Prostate cancer specific antigen P703P #4.
 PN US2002192763-A1.
 PD 19-DEC-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIANG/) JIANG Y.
 PA (KALOS/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNETIL P D.
 PA (HOUN/) HOUGHTON R L.
 PA (DBAS/) Y DE BASBOLS C V.
 PA (FOYT/) FOY T M.
 Query Match 34.4%; Score 472.5; DB 4; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1317
 ID ABB95228 standard; protein; 220 AA.
 DE Human P703PDES protein SEQ ID NO 327.
 PN US2002022248-A1.
 PD 21-FEB-2002.
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIANG/) JIANG Y.
 PA (KALOS/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNETIL P D.
 PA (HOUN/) HOUGHTON R L.
 PA (DBAS/) Y DE BASBOLS C V.
 PA (FOYT/) FOY T M.
 Query Match 34.4%; Score 472.5; DB 5; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1318
 ID ABR34340 standard; protein; 220 AA.
 DE Prostate tumour specific protein sequence SEQ ID 327.
 PN WO200289747-A2.
 PD 14-NOV-2002.
 PA (HEND/) HENDERSON R A.
 Query Match 34.4%; Score 472.5; DB 5; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1319
 ID ADB13777 standard; protein; 220 AA.
 DE Human prostate specific protein P703PDES.
 PN US2003185830-A1.
 PD 02-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 34.4%; Score 472.5; DB 7; Length 220;
 Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 RESULT 1320
 ID ADG36193 standard; protein; 220 AA.
 DE Human prostate-specific polypeptide #9.

PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 34.4%; Score 472.5; DB 7; Length 220;
Best Local Similarity 43.8%; Pred. No. 1.4e-28;
RESULT 1321
ID ADI39732 standard; protein; 262 AA.
DE Human glandular kallikrein (HK2) protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCT.
Query Match 34.4%; Score 472.5; DB 8; Length 262;
Best Local Similarity 36.9%; Pred. No. 1.6e-28;
RESULT 1322
ID ADI37156 standard; protein; 262 AA.
DE Human glandular kallikrein (hHK2) protein.
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Query Match 34.4%; Score 472.5; DB 8; Length 262;
Best Local Similarity 38.9%; Pred. No. 1.6e-28;
RESULT 1323
ID ABR96163 standard; protein; 274 AA.
DE Human NOV12a protein SEQ ID NO:68.
PN WO200290568-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 34.4%; Score 472.5; DB 6; Length 274;
Best Local Similarity 40.7%; Pred. No. 1.7e-28;
RESULT 1324
ID AAP92314 standard; protein; 245 AA.
DE Human recombinant kallikrein gene.
PN EP297913-A.
PD 04-JAN-1989.
PA (AMGE-) AMGEN.
Query Match 34.3%; Score 471; DB 1; Length 245;
Best Local Similarity 40.2%; Pred. No. 2e-28;
RESULT 1325
ID AAB21313 standard; protein; 255 AA.
DE Human PSA.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 34.2%; Score 470.5; DB 3; Length 255;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1326
ID AAU06276 standard; protein; 257 AA.
DE Prostate specific Antigen (PSA) polypeptide.
PN WO200145728-A2.
PD 28-JUN-2001.
PA (EPIM-) EPIMUNE INC.
Query Match 34.2%; Score 470.5; DB 4; Length 257;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1327
ID AAM13649 standard; protein; 261 AA.
DE Human prostatic specific antigen.
PN WO9711172-A1.
PD 27-MAR-1997.
PA (WORC-) WORCESTER FOUNDD BIOMEDICAL RES.
Query Match 34.2%; Score 470.5; DB 2; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1328
ID AAY56048 standard; protein; 261 AA.
DE Human prostate-specific antigen.
PN WO9961068-A1.
PD 02-DEC-1999.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 34.2%; Score 470.5; DB 3; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1329
ID AAY77842 standard; protein; 261 AA.
DE Human prostate-specific antigen (PSA) sequence.
PN WO9960984-A2.
PD 02-DEC-1999.
PA (ENTR-) ENTREMED INC.
Query Match 34.2%; Score 470.5; DB 3; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1330
ID AAB21317 standard; protein; 261 AA.
DE Human PSA.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 34.2%; Score 470.5; DB 3; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1331
ID AAB74821 standard; protein; 261 AA.
DE Prostate tumour antigen amino acid sequence for PSA.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1332
ID AAG62144 standard; protein; 261 AA.
DE Human prostate specific membrane antigen SEQ ID NO: 327.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1333
ID AAG62146 standard; protein; 261 AA.
DE Human prostate specific antigen SEQ ID NO: 329.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1334
ID ABR71859 standard; protein; 261 AA.
DE Human prostatic specific membrane antigen (PSMA).
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUN/) HOUGHTON R L.
PA (DBAS/) Y DE BASOLS C V.
PA (FOYT/) FOY T M.
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1335
ID ABR74202 standard; protein; 261 AA.
DE Human PSA protein SEQ ID NO:78.
PN WO200281646-A2.
PD 17-OCT-2002.
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
Query Match 34.2%; Score 470.5; DB 6; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;

RESULT 1336
ID ADB82777 standard; protein; 261 AA.
DE Human protein sequence useful for the treatment of cancer (SeqID 1558).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE) HYSEQ INC.
Query Match
Best Local Similarity 34.2%; Score 470.5; DB 7; Length 261;
Pred. No. 2.3e-28;
RESULT 1337
ID AAC09580 standard; protein; 261 AA.
DE PSA protein #SEQ ID 78.
PN WO2003008537-A2.
PD 30-JAN-2003.
PA (CTLI) CTL IMMUNOTHERAPIES CORP.
Query Match
Best Local Similarity 34.2%; Score 470.5; DB 7; Length 261;
Pred. No. 2.3e-28;
RESULT 1338
ID ADJ59022 standard; protein; 261 AA.
DE Human PSA precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 34.2%; Score 470.5; DB 7; Length 261;
Pred. No. 2.3e-28;
RESULT 1339
ID ADI39733 standard; protein; 261 AA.
DE Human prostate specific antigen (PSA) protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR) UNIV ARKANSAS MEDICAL SCI.
Query Match
Best Local Similarity 34.2%; Score 470.5; DB 8; Length 261;
Pred. No. 2.3e-28;
RESULT 1340
ID ADI37157 standard; protein; 261 AA.
DE Human prostate specific antigen (hPSA).
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR) UNIV ARKANSAS.
Query Match
Best Local Similarity 34.2%; Score 470.5; DB 8; Length 261;
Pred. No. 2.3e-28;
RESULT 1341
ID ADM72819 standard; protein; 261 AA.
DE Human PSA protein SEQ ID NO:78.
PN WO2004022709-A2.
PD 18-MAR-2004.
PA (MANN) MANNKIND CORP.
Query Match
Best Local Similarity 34.2%; Score 470.5; DB 8; Length 261;
Pred. No. 2.3e-28;
RESULT 1342
ID ABM82166 standard; protein; 261 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2109, SEQ:5591.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 34.2%; Score 470.5; DB 8; Length 261;
Pred. No. 2.3e-28;
RESULT 1343
ID AAB08449 standard; protein; 375 AA.
DE A human prostate specific antigen variant polypeptide.
PN WO2000049158-A2.
PD 24-AUG-2000.
PA (COMP) COMPUGEN LTD.
Query Match
Best Local Similarity 34.2%; Score 470.5; DB 3; Length 375;
Pred. No. 3.4e-28;
RESULT 1344
ID AAG62154 standard; protein; 692 AA.
DE Human WTI/PSA fusion protein SEQ ID NO: 357.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI) CORIXA CORP.
Query Match
Best Local Similarity 34.2%; Score 470.5; DB 4; Length 692;
Pred. No. 6.3e-28;

RESULT 1345
ID AAB67545 standard; protein; 284 AA.
DE Amino acid sequence of protease MH2 catalytic domain in PFEK2-6XHIS-TRG.
PN WO200116289-A2.
PD 08-MAR-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Query Match
Best Local Similarity 34.1%; Score 469; DB 4; Length 284;
Pred. No. 3.3e-28;
RESULT 1346
ID ADJ59024 standard; protein; 261 AA.
DE Human PSA precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 34.1%; Score 468.5; DB 7; Length 261;
Pred. No. 3.3e-28;
RESULT 1347
ID AAU74903 standard; protein; 231 AA.
DE Amino acid sequence of P703P mutated-His fusion protein.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 34.0%; Score 467.5; DB 5; Length 231;
Pred. No. 3.5e-28;
RESULT 1348
ID AAU74934 standard; protein; 231 AA.
DE Amino acid sequence of P703P mutated-His fusion protein.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 34.0%; Score 467.5; DB 5; Length 231;
Pred. No. 3.5e-28;
RESULT 1349
ID AAU72521 standard; protein; 312 AA.
DE NSI-P703P mutated-His fusion protein.
PN WO200104143-A2.
PD 18-JAN-2001.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 34.0%; Score 467.5; DB 4; Length 312;
Pred. No. 4.8e-28;
RESULT 1350
ID AAU74767 standard; protein; 312 AA.
DE Amino acid sequence of NSI-P703 mutated-His fusion protein.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 34.0%; Score 467.5; DB 5; Length 312;
Pred. No. 4.8e-28;
RESULT 1351
ID AAU74928 standard; protein; 312 AA.
DE Amino acid sequence of NSI-P703P mutated-His fusion protein.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 34.0%; Score 467.5; DB 5; Length 312;
Pred. No. 4.8e-28;
RESULT 1352
ID AAP81243 standard; protein; 247 AA.
DE Human spleen trypsin III (trypsinogen III).
PN JP63160582-A.
PD 04-JUL-1988.
PA (SANY) SANKYO CO LTD.
Query Match
Best Local Similarity 34.0%; Score 467; DB 1; Length 247;
Pred. No. 4.1e-28;
RESULT 1353
ID AAR82703 standard; protein; 247 AA.
DE Human pancreatic trypsin III.
PN JP07184655-A.
PD 25-JUL-1995.
PA (SANY) SANKYO CO LTD.
Query Match
Best Local Similarity 34.0%; Score 467; DB 2; Length 247;
Pred. No. 4.1e-28;

RESULT 1354
ID AD59026 standard; protein; 261 AA.
DE Human PSA analogue (Y154) precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (US\$H) US DEPT HEALTH & HUMAN SERVICES.
Query Match 34.0%; Score 466.5; DB 7; Length 261;
Best Local Similarity 40.4%; Pred. No. 4.7e-28;
RESULT 1355
ID ABB84422 standard; peptide; 226 AA.
DE Rat SCCE protein N-terminal fragment SEQ ID 48.
PN WO200262135-A2.
PD 15-AUG-2002.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
Query Match 33.8%; Score 464.5; DB 5; Length 226;
Best Local Similarity 42.7%; Pred. No. 5.8e-28;
RESULT 1356
ID AD59028 standard; protein; 261 AA.
DE Human PSA analogue (L155/Y154) precursor protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (US\$H) US DEPT HEALTH & HUMAN SERVICES.
Query Match 33.8%; Score 464.5; DB 7; Length 261;
Best Local Similarity 40.4%; Pred. No. 6.8e-28;
RESULT 1357
ID AD50549 standard; protein; 237 AA.
DE Rhesus macaque prostate specific antigen (PSA/KLK3) , SEQ ID NO:4.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Query Match 33.8%; Score 464; DB 6; Length 237;
Best Local Similarity 42.6%; Pred. No. 6.7e-28;
RESULT 1358
ID ADM12395 standard; protein; 261 AA.
DE Human prostate-specific antigen protein.
PN US2003235594-A1.
PD 25-DEC-2003.
PA (ANTT-) ANTIGEN EXPRESS INC.
Query Match 33.7%; Score 463.5; DB 8; Length 261;
Best Local Similarity 40.0%; Pred. No. 8.1e-28;
RESULT 1359
ID AD66638 standard; protein; 248 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 131 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 33.7%; Score 462.5; DB 8; Length 248;
Best Local Similarity 40.2%; Pred. No. 9.2e-28;
RESULT 1360
ID AD66637 standard; protein; 248 AA.
DE Human prostatic carcinoma derived protein SEQ ID 131 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 33.7%; Score 462.5; DB 8; Length 248;
Best Local Similarity 40.2%; Pred. No. 9.2e-28;
RESULT 1361
ID AD66634 standard; protein; 251 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 232 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 33.7%; Score 462.5; DB 8; Length 248;
Best Local Similarity 40.2%; Pred. No. 9.2e-28;
RESULT 1362
ID AD66636 standard; protein; 251 AA.
DE Human prostatic carcinoma derived protein SEQ ID 232 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 33.7%; Score 462.5; DB 8; Length 251;
Best Local Similarity 40.2%; Pred. No. 9.3e-28;
RESULT 1363
ID ADP27546 standard; protein; 281 AA.
DE Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Query Match 33.6%; Score 462; DB 8; Length 281;
Best Local Similarity 41.0%; Pred. No. 1.1e-27;
RESULT 1364
ID ADP27545 standard; protein; 297 AA.
DE Human kallikrein-3 (KLK-3) EHT103 protien a variant SeqID 19.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Query Match 33.6%; Score 462; DB 8; Length 297;
Best Local Similarity 41.0%; Pred. No. 1.2e-27;
RESULT 1365
ID AAR84668 standard; protein; 261 AA.
DE Prepro-hk2 kallikrein.
PN WO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 33.5%; Score 460.5; DB 2; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.4e-27;
RESULT 1366
ID AAW10600 standard; protein; 261 AA.
DE Human prepro-Trip26-glandular kallikrein-2.
PN WO9701630-A1.
PD 16-JAN-1997.
PA (ORIN) ORION YHTYMAE OY.
Query Match 33.5%; Score 460.5; DB 2; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.4e-27;
RESULT 1367
ID AAU98921 standard; protein; 245 AA.
DE Human prostate specific antigen (PSA) variant.
PN WO200240059-A2.
PD 23-MAY-2002.
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
PA (MINC/) MINCHEFF M S.
PA (LOUK/) LOUKINOV D I.
PA (ZOUB/) ZOUBAK S.
Query Match 33.4%; Score 459.5; DB 5; Length 245;
Best Local Similarity 41.4%; Pred. No. 1.5e-27;
RESULT 1368
ID AAY08894 standard; protein; 238 AA.
DE Chimeric serine protease FXT protein.
PN EP927764-A2.
PD 07-JUL-1999.
PA (HOPF) ROCHE DIAGNOSTICS GMBH.
Query Match 33.4%; Score 459; DB 2; Length 238;
Best Local Similarity 40.5%; Pred. No. 1.6e-27;
RESULT 1369
ID AAB21314 standard; protein; 255 AA.
DE Human KLK2.
PN WO200053776-A2.
PD 14-SEP-2000.

PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 33.4%; Score 458.5; DB 3; Length 255;
Best Local Similarity 40.8%; Pred. No. 1.9e-27;
RESULT 1370
ID AAW06971 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein prepro-hk2.
PN WO9634964-A2.
PD 07-NOV-1996.
PA (HYBR-) HYBRITTECH INC.
PA (MAYO-) MAYO FOUNDATION.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1371
ID AAW83303 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein protein pphk2.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1372
ID AAW49085 standard; protein; 261 AA.
DE Wild-type human kallikrein 2 (hk2).
PN WO9821365-A2.
PD 22-MAY-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1373
ID AAW45397 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein precursor prepro-hk2.
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1374
ID AAW96189 standard; protein; 261 AA.
DE Prepro human kallikrein 2 (preprohk2).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG/) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
ID AAB21318 standard; protein; 261 AA.
DE Human KLK2.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 33.4%; Score 458.5; DB 3; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1376
ID AAW06279 standard; protein; 261 AA.
DE Human kallikrein2 polypeptide.
PN WO200145728-A2.
PD 28-JUN-2001.
PA (EPIM-) EPIMUNE INC.
Query Match 33.4%; Score 458.5; DB 4; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1377
ID ADB75390 standard; protein; 261 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 33.4%; Score 458.5; DB 7; Length 261;

Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1378
ID AAW83213 standard; protein; 237 AA.
DE Prostate-specific antigen protein hk3.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match 33.3%; Score 457.5; DB 2; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1379
ID AAW56086 standard; protein; 237 AA.
DE Human prostate specific antigen protein.
PN WO9810292-A1.
PD 12-MAR-1998.
PA (CENZ) CENTOCOR INC.
Query Match 33.3%; Score 457.5; DB 2; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1380
ID AAW96187 standard; protein; 237 AA.
DE Human prostate specific antigen (PSA).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG/) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Query Match 33.3%; Score 457.5; DB 2; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1381
ID AAB11041 standard; peptide; 237 AA.
DE Human prostate-specific antigen N-terminal fragment #2.
PN EP1043394-A2.
PD 11-OCT-2000.
PA (SERA-) SERATEC GBS BIOTECHNOLOGIE MBH.
Query Match 33.3%; Score 457.5; DB 3; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1382
ID AAB19819 standard; protein; 237 AA.
DE Prostate specific antigen specific to benign prostatic hyperplasia.
PN WO200067030-A1.
PD 09-NOV-2000.
PA (HYBR-) HYBRITTECH INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 33.3%; Score 457.5; DB 4; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1383
ID AAB19818 standard; protein; 237 AA.
DE Prostate specific antigen elevated in benign prostatic hyperplasia.
PN WO200066718-A1.
PD 09-NOV-2000.
PA (HYBR-) HYBRITTECH INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 33.3%; Score 457.5; DB 4; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1384
ID ADA50546 standard; protein; 237 AA.
DE Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Query Match 33.3%; Score 457.5; DB 6; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1385
ID ADA09840 standard; protein; 237 AA.
DE Human mature prostate specific antigen (PSA).
PN US2003059864-A1.
PD 27-MAR-2003.
PA (MIKO/) MIKOLAJCZYK S D.
PA (RITT/) RITTENHOUSE H G.
Query Match 33.3%; Score 457.5; DB 6; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1386

ID ADJ59023 standard; protein; 237 AA.
DE Human PSA mature protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 33.3%; Score 457.5; DB 7; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1387
ID ADF60980 standard; protein; 237 AA.
DE Human prostate specific antigen (PSA).
PN US2003166036-A1.
PD 04-SEP-2003.
PA (MIKO/) MIKOLAJCZYK S D.
PA (RITT/) RITTENHOUSE H G.
Query Match 33.3%; Score 457.5; DB 8; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1388
ID AAF70677 standard; protein; 245 AA.
DE Human kallikrein gene product.
PN WO8702709-A.
PD 07-MAY-1987.
PA (BIOT-) BIOTECHN RES PARTN.
PA (CALB-) CALIF BIOTECHNOL INC.
Query Match 33.2%; Score 456; DB 1; Length 245;
Best Local Similarity 39.7%; Pred. No. 2.9e-27;
RESULT 1389
ID AAW5398 standard; protein; 237 AA.
DE Prostate-specific antigen protein HK3 (PSA).
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 33.2%; Score 455.5; DB 2; Length 237;
Best Local Similarity 41.6%; Pred. No. 3e-27;
RESULT 1390
ID ADJ59025 standard; protein; 237 AA.
DE Human PSA mature protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 33.2%; Score 455.5; DB 7; Length 237;
Best Local Similarity 41.6%; Pred. No. 3e-27;
RESULT 1391
ID AAW06972 standard; protein; 261 AA.
DE Kallikrein prepro-hk2v217 variant.
PN WO9634964-A2.
PD 07-NOV-1996.
PA (HYBR-) HYBRITTECH INC.
PA (MAYO-) MAYO FOUNDATION.
Query Match 33.2%; Score 455.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 3.3e-27;
RESULT 1392
ID AAW45400 standard; protein; 261 AA.
DE Prostate-specific glandular kallikrein hk2v217.
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 33.2%; Score 455.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 3.3e-27;
RESULT 1393
ID AAW59129 standard; protein; 232 AA.
DE Homo sapiens Tubb Interactor (TIT-1) protein.
PN WO9812302-A1.
PD 26-MAR-1998.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 33.1%; Score 454.5; DB 2; Length 232;
Best Local Similarity 43.8%; Pred. No. 3.5e-27;
RESULT 1394
ID AAT72523 standard; protein; 232 AA.
DE Human prostate antigen #1.
PN WO20010413-A2.
PD 18-JAN-2001.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Query Match 33.1%; Score 454.5; DB 4; Length 232;
Best Local Similarity 43.8%; Pred. No. 3.5e-27;
RESULT 1395
ID AAT74769 standard; protein; 232 AA.
DE Protein sequence of prostate homologue #1.
PN WO200200708-A2.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 33.1%; Score 454.5; DB 5; Length 232;
Best Local Similarity 43.8%; Pred. No. 3.5e-27;
RESULT 1396
ID AAT74930 standard; protein; 232 AA.
DE Amino acid sequence of prostate protein fragment #1.
PN WO200200867-A1.
PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 33.1%; Score 454.5; DB 5; Length 232;
Best Local Similarity 43.8%; Pred. No. 3.5e-27;
RESULT 1397
ID AAR84669 standard; protein; 244 AA.
DE Pro-hk2 kallikrein.
PN WO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 33.1%; Score 454.5; DB 2; Length 244;
Best Local Similarity 41.2%; Pred. No. 3.7e-27;
RESULT 1398
ID ADO38617 standard; protein; 261 AA.
DE Prostate Specific Antigen (PSA).
PN US2004058861-A1.
PD 25-MAR-2004.
PA (ANTT-) ANTIGEN EXPRESS INC.
Query Match 33.1%; Score 454.5; DB 8; Length 261;
Best Local Similarity 39.6%; Pred. No. 4e-27;
RESULT 1399
ID ADJ59027 standard; protein; 237 AA.
DE Human PSA analogue (Y154) mature protein sequence.
PN WO2003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 33.0%; Score 453.5; DB 7; Length 237;
Best Local Similarity 41.6%; Pred. No. 4.3e-27;
RESULT 1400
ID AAW83204 standard; protein; 244 AA.
DE Prostate-specific glandular kallikrein protein phk2.
PN WO9846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match 32.9%; Score 452.5; DB 2; Length 244;
Best Local Similarity 41.8%; Pred. No. 5.3e-27;
RESULT 1401
ID AAW45396 standard; protein; 244 AA.
DE Prostate-specific glandular kallikrein precursor pro-hk2.
PN WO9802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 32.9%; Score 452.5; DB 2; Length 244;
Best Local Similarity 41.8%; Pred. No. 5.3e-27;
RESULT 1402
ID AAW96188 standard; protein; 244 AA.
DE Pro human Kallikrein 2 (prohk2).
PN WO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Query Match 32.9%; Score 452.5; DB 2; Length 244;

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Best Local Similarity 41.8%; Pred. No. 5.3e-27;
RESULT 1403
ID AAM03130 standard; protein; 250 AA.
DE Prostate-specific antigen.
PN W09621042-A2.
PD 11-JUL-1996.
PA (UYBO-) UNIV BOSTON.
Query Match
Best Local Similarity 32.9%; Score 452.5; DB 2; Length 250;
Pred. No. 5.4e-27;
RESULT 1404
ID ADP27538 standard; protein; 281 AA.
DE Human kallikrein-2 (KLK-2) EHT102 protein b variant SegID 12.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Query Match
Best Local Similarity 32.9%; Score 452.5; DB 8; Length 281;
Pred. No. 6.1e-27;
RESULT 1405
ID ADP27537 standard; protein; 297 AA.
DE Human kallikrein-2 (KLK-2) EHT102 protein a variant SegID 11.
PN FR2848569-A1.
PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Query Match
Best Local Similarity 32.9%; Score 452.5; DB 8; Length 297;
Pred. No. 6.5e-27;
RESULT 1406
ID ADJ59029 standard; protein; 236 AA.
DE Human PSA analogue (L155/Y154) mature protein sequence.
PN W02003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 32.9%; Score 451.5; DB 7; Length 236;
Pred. No. 6.1e-27;
RESULT 1407
ID AAR77098 standard; protein; 237 AA.
DE Prostate-specific antigen.
PN W09528498-A1.
PD 26-OCT-1995.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match
Best Local Similarity 32.8%; Score 450.5; DB 2; Length 237;
Pred. No. 7.4e-27;
RESULT 1408
ID AAM63202 standard; protein; 237 AA.
DE Prostate-specific glandular kallikrein protein hK2.
PN W09846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match
Best Local Similarity 32.8%; Score 450.5; DB 2; Length 237;
Pred. No. 7.4e-27;
RESULT 1409
ID AAM45395 standard; protein; 237 AA.
DE Mature prostate-specific glandular kallikrein hK2.
PN W09802748-A1.
PD 22-JAN-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match
Best Local Similarity 32.8%; Score 450.5; DB 2; Length 237;
Pred. No. 7.4e-27;
RESULT 1410
ID AAM96186 standard; protein; 237 AA.
DE Mature human kallikrein 2 (hK2).
PN W09859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUNG) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Query Match
Best Local Similarity 32.8%; Score 450.5; DB 2; Length 237;
Pred. No. 7.4e-27;
RESULT 1411
ID ADJ50561 standard; protein; 237 AA.
DE Kallikrein KLK2, SEQ ID NO:16.

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PN W02003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Query Match
Best Local Similarity 32.8%; Score 450.5; DB 6; Length 237;
Pred. No. 7.4e-27;
RESULT 1412
ID AAR84667 standard; protein; 237 AA.
DE Mature kallikrein hK2.
PN W09530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match
Best Local Similarity 32.6%; Score 448.5; DB 2; Length 237;
Pred. No. 1e-26;
RESULT 1413
ID ADI17277 standard; protein; 217 AA.
DE Polypeptide homologous to a human NOVX domain SegID 813.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 32.6%; Score 447.5; DB 5; Length 217;
Pred. No. 1.1e-26;
RESULT 1414
ID ADI17269 standard; protein; 217 AA.
DE Polypeptide homologous to a human NOVX domain SegID 805.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 32.6%; Score 447.5; DB 5; Length 217;
Pred. No. 1.1e-26;
RESULT 1415
ID ADJ83076 standard; protein; 217 AA.
DE Trypsin protein which is related to human NOVX protein - SEQ ID 67.
PN U23003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERRHUSEN B D.
PA (PATY/) PATYURAJAN M.
PA (LEPL/) LEFLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERS E S.
PA (VERN/) VERNET C A M.
PA (LITL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (PERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match
Best Local Similarity 32.6%; Score 447.5; DB 7; Length 217;
Pred. No. 1.1e-26;
RESULT 1416
ID AAM63212 standard; protein; 237 AA.
DE hK2 variant A217V.
PN W09846795-A1.
PD 22-OCT-1998.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Query Match
Best Local Similarity 32.6%; Score 447.5; DB 2; Length 237;
Pred. No. 1.3e-26;
RESULT 1417

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ID AAW49087 standard; protein; 237 AA.
DE Mutant human Kallikrein 2 (hk2) A217V.
PN MO9821365-A2.
PD 22-MAY-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 32.6%; Score 447.5; DB 2; Length 237;
Best Local Similarity 42.0%; Pred. No. 1.3e-26;
RESULT 1418
ID AAW96190 standard; protein; 237 AA.
DE Variant human Kallikrein 2 (hk2).
PN MO9859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUN-) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Query Match 32.6%; Score 447.5; DB 2; Length 237;
Best Local Similarity 42.0%; Pred. No. 1.3e-26;
RESULT 1419
ID AAW11023 standard; protein; 240 AA.
DE Human prostate specific antigen.
PN MO9640754-A1.
PD 19-DEC-1996.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 32.4%; Score 445; DB 2; Length 240;
Best Local Similarity 41.0%; Pred. No. 2e-26;
RESULT 1420
ID AAR84671 standard; protein; 237 AA.
DE Mature kallikrein hk3.
PN MO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 32.4%; Score 444.5; DB 2; Length 237;
Best Local Similarity 41.1%; Pred. No. 2.1e-26;
RESULT 1421
ID AAW82643 standard; protein; 227 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:2892.
PN WO2004023373-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 32.2%; Score 443; DB 8; Length 227;
Best Local Similarity 39.6%; Pred. No. 2.7e-26;
RESULT 1422
ID AAR84670 standard; protein; 238 AA.
DE Mature kallikrein hk2.
PN MO9530758-A1.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITTECH INC.
Query Match 32.1%; Score 441.5; DB 2; Length 238;
Best Local Similarity 40.9%; Pred. No. 3.6e-26;
RESULT 1423
ID AAR94526 standard; protein; 279 AA.
DE Korean viper Salmosa thrombin-like protease, Halypin.
PN EP070767-A2.
PD 17-APR-1996.
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
Query Match 32.0%; Score 439; DB 2; Length 279;
Best Local Similarity 37.7%; Pred. No. 6.7e-26;
RESULT 1424
ID AAG79000 standard; protein; 233 AA.
DE Mannuishi fibrinolytic enzyme, brevinase.
PN KR2001045716-A.
PD 05-JUN-2001.
PA (LEEJ/) LEE J W.
PA (PARK/) PARK W.
Query Match 31.8%; Score 436.5; DB 4; Length 233;
Best Local Similarity 37.9%; Pred. No. 8.7e-26;
RESULT 1425
ID AAM52944 standard; protein; 260 AA.
DE Agkistrodon halys brevicaudus thrombin-like protease, salmobin.

PN KR98002267-A.
PD 30-MAR-1998.
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
Query Match 31.7%; Score 436; DB 2; Length 260;
Best Local Similarity 36.1%; Pred. No. 1.1e-25;
RESULT 1426
ID AAB50447 standard; protein; 205 AA.
DE Human prostate cancer-related intracellular protein #1.
PN WO200071711-A2.
PD 30-NOV-2000.
PA (SAAT/) SAATCIOGLU F.
Query Match 31.4%; Score 431.5; DB 4; Length 205;
Best Local Similarity 44.2%; Pred. No. 1.8e-25;
RESULT 1427
ID ADE78966 standard; protein; 227 AA.
DE Human protein modification and maintenance molecule (PMM) -4.
PN WO2003063688-A2.
PD 07-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 31.3%; Score 430; DB 7; Length 227;
Best Local Similarity 39.2%; Pred. No. 2.7e-25;
RESULT 1428
ID AAW69388 standard; protein; 205 AA.
DE Prostate tumour specific gene clone DE13 protein.
PN MO9837418-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 2; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1429
ID AAW71872 standard; protein; 205 AA.
DE Protein encoded by prostate tumour clone P703 splice variant DE13.
PN MO9837093-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 2; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1430
ID AAY82005 standard; protein; 205 AA.
DE Human immunogenic prostate tumour protein sequence SEQ ID NO:176.
PN WO200004149-A2.
PD 27-JAN-2000.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 3; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1431
ID AAB94414 standard; protein; 205 AA.
DE Human prostate tumour protein partial variant sequence #2.
PN US2002090372-A1.
PD 11-JUL-2002.
PA (XUUJ/) XU J.
PA (DILL/) DILLON D C.
Query Match 31.0%; Score 426.5; DB 3; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1432
ID AAM01120 standard; protein; 205 AA.
DE Human prostate-specific amino acid sequence P703P-DE13.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 4; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1433
ID AAV69766 standard; protein; 205 AA.
DE Human prostate cDNA encoded protein #6.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 31.0%; Score 426.5; DB 4; Length 205;
Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1434
ID AAB74803 standard; protein; 205 AA.
DE Prostate tumour antigen predicted amino acid sequence for P703P-DE13.

PN W0200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 31.0%; Score 426.5; DB 4; Length 205;
Pred. No. 4.5e-25;
RESULT 1435
ID AAG99005 standard; protein; 205 AA.
DE Human prostate-specific amino acid sequence P703P-DE13.
PN W0200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 31.0%; Score 426.5; DB 4; Length 205;
Pred. No. 4.5e-25;
RESULT 1436
ID ABU71656 standard; protein; 205 AA.
DE Prostate cancer specific antigen P703P #2.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HONG/) HONGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
Best Local Similarity 31.0%; Score 426.5; DB 4; Length 205;
Pred. No. 4.5e-25;
RESULT 1437
ID AAU04964 standard; protein; 205 AA.
DE Human prostate tumour protein DE13.
PN US6262245-B1.
PD 17-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 31.0%; Score 426.5; DB 4; Length 205;
Pred. No. 4.5e-25;
RESULT 1438
ID ABB95225 standard; protein; 205 AA.
DE Human P703P-DE13 protein SEQ ID NO 176.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
Query Match
31.0%; Score 426.5; DB 5; Length 205;

Best Local Similarity 43.7%; Pred. No. 4.5e-25;
RESULT 1439
ID ABG76668 standard; protein; 205 AA.
DE Prostate tumour protein #6.
PN US2002081580-A1.
PD 27-JUN-2002.
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
Query Match
Best Local Similarity 31.0%; Score 426.5; DB 5; Length 205;
Pred. No. 4.5e-25;
RESULT 1440
ID ABR54337 standard; protein; 205 AA.
DE Prostate tumour specific protein sequence SEQ ID 176.
PN W0200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 31.0%; Score 426.5; DB 6; Length 205;
Pred. No. 4.5e-25;
RESULT 1441
ID ADB13626 standard; protein; 205 AA.
DE Human prostate specific protein P703P-DE13.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 31.0%; Score 426.5; DB 7; Length 205;
Pred. No. 4.5e-25;
RESULT 1442
ID ADG26042 standard; protein; 205 AA.
DE Human prostate-specific polypeptide #6.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 31.0%; Score 426.5; DB 7; Length 205;
Pred. No. 4.5e-25;
RESULT 1443
ID ABB09589 standard; protein; 234 AA.
DE Deinagkistrodon acutus venom thrombin-like protein (234 residue variant).
PN CN1181421-A.
PD 13-MAY-1998.
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
Query Match
Best Local Similarity 30.7%; Score 422.5; DB 5; Length 234;
Pred. No. 1e-24;
RESULT 1444
ID ADK36957 standard; protein; 281 AA.
DE Novel human polypeptide SeqID9039.
PN W0200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSIQ INC.
Query Match
Best Local Similarity 30.7%; Score 422.5; DB 5; Length 281;
Pred. No. 1.3e-24;
RESULT 1445
ID ABU92024 standard; protein; 218 AA.
DE Human protein modification and maintenance molecule-4 (PMM-4).
PN W02003031939-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 30.7%; Score 422; DB 6; Length 218;
Pred. No. 1.1e-24;
RESULT 1446
ID AAB31579 standard; peptide; 225 AA.
DE Amino acid sequence of cod tryptsin isozymes.
PN W0200078332-A2.
PD 28-DEC-2000.
PA (BJAR/) BJARNASON J B.
Query Match
Best Local Similarity 30.6%; Score 421; DB 4; Length 225;
Pred. No. 1.3e-24;
RESULT 1447
ID ADE15982 standard; protein; 218 AA.
DE G-coupled protein receptor related polypeptide, SPQ ID No 12.
PN W0200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match
30.6%; Score 420; DB 7; Length 218;

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Best Local Similarity 37.8%; Pred. No. 1.5e-24;
RESULT 1448
ID AD693921 standard; protein; 218 AA.
DE Human G-coupled protein receptor-related protein #6.
PN US2004006205-A1.
PD 08-JAN-2004.
PA (LILU/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILU/) MILLER C E.
PA (SEPT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PEN A/) PEN A C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASW/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTAK K.
PA (PATR/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (MALV/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
Query Match 30.6%; Score 420; DB 8; Length 218;
Best Local Similarity 37.8%; Pred. No. 1.5e-24;
RESULT 1449
ID AAY28641 standard; protein; 207 AA.
DE Human secreted protein from cDNA clone HKAET41.
PN W09940183-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 30.4%; Score 418; DB 2; Length 207;
Best Local Similarity 46.1%; Pred. No. 2e-24;
RESULT 1450
ID AAM46773 standard; protein; 233 AA.
DE Amino acid sequence of Salmomase.
PN EP814164-A2.
PD 29-DEC-1997.
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
Query Match 30.4%; Score 417.5; DB 2; Length 233;
Best Local Similarity 36.6%; Pred. No. 2.5e-24;
RESULT 1451
ID AAE21442 standard; protein; 226 AA.
DE Human trypsin domain consensus protein #2.
PN W0200226802-A2.
PD 04-APR-2002.
PA (MILU-) MILLENNIUM PHARM INC.
Query Match 30.3%; Score 416.5; DB 5; Length 226;
Best Local Similarity 42.6%; Pred. No. 2.9e-24;
RESULT 1452
ID ABG75786 standard; protein; 226 AA.
DE Trypsin domain consensus sequence. SMART.
PN US2002165152-A1.
PD 07-NOV-2002.
PA (KAPE/) KAPFELER-LIBERMAN R.
Query Match 30.3%; Score 416.5; DB 6; Length 226;
Best Local Similarity 42.6%; Pred. No. 2.9e-24;
RESULT 1453
ID ADA05736 standard; protein; 198 AA.
DE Human NOV18c protein SEQ ID NO:96.
PN W02003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.

Query Match 30.0%; Score 412.5; DB 6; Length 198;
Best Local Similarity 36.8%; Pred. No. 5.2e-24;
RESULT 1454
ID ADN62900 standard; protein; 198 AA.
DE Human NOV18c.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILU/) MILLER T.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILU/) LI L.
PA (GUOX/) GUO X.
PA (PATR/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELIE/) ELLERMAN K.
PA (MALV/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATF/) CATERTON E.
PA (JIWU/) JI W.
PA (MILU/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PEN A/) PEN A C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP1/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANCOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 30.0%; Score 412.5; DB 8; Length 198;
Best Local Similarity 36.8%; Pred. No. 5.2e-24;
RESULT 1455
ID ADA50560 standard; protein; 194 AA.
DE Prostate specific antigen (PSA/KLK3), SEQ ID NO:15.
PN W02003031569-A2.
PD 17-APR-2003.
PA (CENZ-) CENTOCOR INC.
Query Match 29.8%; Score 409; DB 6; Length 194;
Best Local Similarity 38.7%; Pred. No. 9.5e-24;
RESULT 1456
ID ADG75684 standard; protein; 215 AA.
DE Human protein modification and maintenance molecule polypeptide SegidB.
PN W02003083084-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 29.8%; Score 409; DB 7; Length 215;
Best Local Similarity 37.1%; Pred. No. 1.1e-23;
RESULT 1457
ID ABM82829 standard; protein; 215 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3076.
PN W02004023873-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 29.8%; Score 409; DB 8; Length 215;
Best Local Similarity 37.1%; Pred. No. 1.1e-23;
RESULT 1458
ID ABM83248 standard; protein; 299 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3497.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
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Query Match
 Best Local Similarity 29.8%; Score 409; DB 8; Length 299;
 RESULT 1459
 ID AAB05738 standard; protein; 181 AA.
 DE Human NOV186 protein SEQ ID NO:98.
 PN W02003029424-A2.
 PD 10-APR-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 29.7%; Score 408.5; DB 6; Length 181;
 RESULT 1460
 ID AAB062902 standard; protein; 181 AA.
 DE Human NOV186.
 PN US2004038223-A1.
 PD 26-FEB-2004.
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEWM/) PEWMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUUU/) JU U.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATR/) PATURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELIE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERRUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIMW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGRE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIRI/) DIRIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 Query Match
 Best Local Similarity 29.7%; Score 408.5; DB 8; Length 181;
 RESULT 1461
 ID AAB062641 standard; protein; 222 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:2890.
 PN W020004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 29.6%; Score 407; DB 8; Length 222;
 RESULT 1462
 ID AAB08510 standard; protein; 230 AA.
 DE A recombinant protein C activator polypeptide.
 PN W0200050612-A2.
 PD 31-AUG-2000.
 PA (INLI-) INSTRUMENTATION LAB.
 Query Match
 Best Local Similarity 29.6%; Score 406.5; DB 3; Length 230;
 RESULT 1463
 ID AAW76538 standard; protein; 231 AA.
 DE A confortriix protein C activator protein fragment.
 PN W09842850-A1.
 PD 01-OCT-1998.
 PA (RPMS-) RPMS TECHNOLOGY LTD.

Query Match
 Best Local Similarity 29.6%; Score 406.5; DB 2; Length 231;
 RESULT 1464
 ID AAB09590 standard; protein; 218 AA.
 DE Deinagkistrodon acutus venom thrombin-like protein (218 residue variant).
 PN CN1181421-A.
 PD 13-MAY-1998.
 PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
 Query Match
 Best Local Similarity 29.5%; Score 405.5; DB 5; Length 218;
 RESULT 1465
 ID AAB04665 standard; protein; 220 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4914.
 PN W020004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 29.5%; Score 405; DB 8; Length 220;
 RESULT 1466
 ID AAB08511 standard; protein; 230 AA.
 DE Biosynthetic variant of protein C activator polypeptide.
 PN W0200050612-A2.
 PD 31-AUG-2000.
 PA (INLI-) INSTRUMENTATION LAB.
 Query Match
 Best Local Similarity 29.4%; Score 403.5; DB 3; Length 230;
 RESULT 1467
 ID AAR20557 standard; protein; 234 AA.
 DE Fibrinogenolytic protein #4 from snake venom.
 PN DE4023699-A.
 PD 30-JAN-1992.
 PA (BADI-) BASF AG.
 Query Match
 Best Local Similarity 29.3%; Score 403; DB 2; Length 234;
 RESULT 1468
 ID AAB81333 standard; protein; 255 AA.
 DE Batroxobin.
 PN JP63049084-A.
 PD 01-MAR-1988.
 PA (YAMA/) YAMASHINA I.
 Query Match
 Best Local Similarity 29.3%; Score 402; DB 1; Length 255;
 RESULT 1469
 ID AAR05436 standard; protein; 255 AA.
 DE Batroxobin gene product.
 PN JP02124092-A.
 PD 11-MAY-1990.
 PA (FUJI-) FUJISAWA PHARM CO LTD.
 Query Match
 Best Local Similarity 29.3%; Score 402; DB 2; Length 255;
 RESULT 1470
 ID AAY17869 standard; protein; 255 AA.
 DE Ataraca batroxobin.
 PN W09929838-A1.
 PD 17-JUN-1999.
 PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
 Query Match
 Best Local Similarity 29.3%; Score 402; DB 2; Length 255;
 RESULT 1471
 ID AAB21441 standard; protein; 249 AA.
 DE Human trypsin domain consensus protein #1.
 PN W0200226802-A2.
 PD 04-APR-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match
 Best Local Similarity 29.2%; Score 401.5; DB 5; Length 249;
 RESULT 1472
 ID AAM52946 standard; protein; 231 AA.
 DE Batroxobin, a snake venom protease.
 PN KR98002267-A.
 PD 30-MAR-1998.
 PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
 Query Match
 Best Local Similarity 29.1%; Score 400; DB 2; Length 231;

Best Local Similarity 34.2%; Pred. No. 5.6e-23;
RESULT 1473
ID AAB11711 standard; protein; 264 AA.
DE Mouse serine protease BSSPS (mbssps) SEQ ID NO:4.
PN WO20031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 28.8%; Score 395.5; DB 3; Length 264;
Best Local Similarity 39.1%; Pred. No. 1.4e-22;
RESULT 1474
ID AAM52945 standard; protein; 236 AA.
DE Flaboboxin, a snake venom protease.
PN KR98002267-A.
PD 30-MAR-1998.
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
Query Match 28.7%; Score 394; DB 2; Length 236;
Best Local Similarity 36.8%; Pred. No. 1.7e-22;
RESULT 1475
ID AAR20556 standard; protein; 236 AA.
DE Fibrinogenolytic protein #3 from snake venom.
PN DE4023699-A.
PD 30-JAN-1992.
PA (BADI) BASF AG.
Query Match 28.6%; Score 393; DB 2; Length 236;
Best Local Similarity 37.3%; Pred. No. 2e-22;
RESULT 1476
ID ABM82831 standard; protein; 233 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3080.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 28.5%; Score 392; DB 8; Length 233;
Best Local Similarity 36.8%; Pred. No. 2.3e-22;
RESULT 1477
ID AAE39993 standard; protein; 253 AA.
DE Human adipisin protein #2.
PN US2003092620-A1.
PD 15-MAY-2003.
PA (GENST) GENSET SA.
Query Match 28.5%; Score 391; DB 7; Length 253;
Best Local Similarity 36.0%; Pred. No. 3e-22;
RESULT 1478
ID ABG5785 standard; protein; 227 AA.
DE Trypsin domain consensus sequence. PRAM.
PN US2002165152-A1.
PD 07-NOV-2002.
PA (KAPF/) KAPFILLER-LIBERMANN R.
Query Match 28.3%; Score 389; DB 6; Length 227;
Best Local Similarity 40.4%; Pred. No. 3.9e-22;
RESULT 1479
ID ADE58223 standard; protein; 253 AA.
DE Human protein P00746, SEQ ID NO 4094.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 28.3%; Score 389; DB 7; Length 253;
Best Local Similarity 38.5%; Pred. No. 4.3e-22;
RESULT 1480
ID AAP70758 standard; protein; 269 AA.
DE Pig pancreas elastase-2.
PN JP62000276-A.
PD 06-JAN-1987.
PA (SANY) SANKYO CO LTD.
Query Match 28.2%; Score 388; DB 1; Length 269;
Best Local Similarity 38.5%; Pred. No. 5.5e-22;
RESULT 1481
ID AAE39993 standard; protein; 253 AA.
DE Human adipisin protein #1.
PN US2003092620-A1.
PD 15-MAY-2003.
PA (GENST) GENSET SA.
Query Match 28.2%; Score 387; DB 7; Length 253;

Best Local Similarity 38.5%; Pred. No. 6.2e-22;
RESULT 1482
ID AAB11710 standard; protein; 264 AA.
DE Human serine protease BSSPS (mbssps) SEQ ID NO:2.
PN WO20031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 28.1%; Score 386.5; DB 3; Length 264;
Best Local Similarity 36.8%; Pred. No. 7e-22;
RESULT 1483
ID ABR39439 standard; protein; 264 AA.
DE Human GENSET polypeptide clone name vCTRL-1.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GENST) GENSET SA.
Query Match 28.1%; Score 386.5; DB 6; Length 264;
Best Local Similarity 36.8%; Pred. No. 7e-22;
RESULT 1484
ID ABU09382 standard; protein; 271 AA.
DE Consensus sequence of trypsin-like domain.
PN WO2003031463-A2.
PD 17-APR-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 28.1%; Score 386; DB 6; Length 271;
Best Local Similarity 39.1%; Pred. No. 7.9e-22;
RESULT 1485
ID ABM82830 standard; protein; 212 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3079.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 28.1%; Score 385.5; DB 8; Length 212;
Best Local Similarity 36.3%; Pred. No. 6.7e-22;
RESULT 1486
ID ABM82644 standard; protein; 212 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2893.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 28.1%; Score 385.5; DB 8; Length 212;
Best Local Similarity 36.3%; Pred. No. 6.7e-22;
RESULT 1487
ID ABM81778 standard; protein; 264 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GEHT) GENENTECH INC.
Query Match 28.1%; Score 385.5; DB 8; Length 264;
Best Local Similarity 36.8%; Pred. No. 8.4e-22;
RESULT 1488
ID ADR66037 standard; protein; 213 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILASKY C.
Query Match 28.0%; Score 385; DB 8; Length 213;
Best Local Similarity 40.2%; Pred. No. 7.4e-22;
RESULT 1489
ID ADR66935 standard; protein; 213 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 233 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILASKY C.
Query Match 28.0%; Score 385; DB 8; Length 213;
Best Local Similarity 40.2%; Pred. No. 7.4e-22;

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RESULT 1490
ID AAB61724 standard; protein; 269 AA.
DE Porcine elastase II.
PN JP61192289-A.
PD 26-FEB-1986.
PA (KIRI ) KIRIN BREWERY KK.
Query Match
Best Local Similarity 27.9%; Score 384; DB 1; Length 269;
RESULT 1491
ID AAR07513 standard; protein; 258 AA.
DE Ancrod-like polypeptide #2.
PN EP395375-A.
PD 31-OCT-1990.
PA (GLAX ) GLAXO INC.
PA (KNOL ) KNOLL AG.
Query Match
Best Local Similarity 27.9%; Score 383; DB 2; Length 258;
RESULT 1492
ID AAR05775 standard; protein; 272 AA.
DE Snake venom ancrod polypeptide.
PN WO9006362-A.
PD 14-JUN-1990.
PA (BADI ) BASF AG.
PA (BACH ) BACH A.
Query Match
Best Local Similarity 27.9%; Score 383; DB 2; Length 272;
RESULT 1493
ID AAU79393 standard; protein; 171 AA.
DE Novel human kallikrein KLK15, splice variant #3.
PN WO200214485-A2.
PD 21-FEB-2002.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 27.8%; Score 382.5; DB 5; Length 171;
RESULT 1494
ID ADN10933 standard; protein; 171 AA.
DE Human kallikrein 15, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 27.8%; Score 382.5; DB 8; Length 171;
RESULT 1495
ID ABM62642 standard; protein; 212 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2891.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY ) INCYTE CORP.
Query Match
Best Local Similarity 27.8%; Score 382; DB 8; Length 212;
RESULT 1496
ID AAR05772 standard; protein; 250 AA.
DE Human adipisin gene product from the clone phg31.
PN WO9006365-A.
PD 14-JUN-1990.
PA (BETH ) BETH ISRAEL HOSPITAL ASSOC.
PA (DANA ) DANA-FARBER CANCER INST.
PA (METR ) METABOLIC BIOSYSTEMS INC.
PA (BETH ) BETH ISRAEL HOSPITAL ASSOC.
Query Match
Best Local Similarity 27.8%; Score 382; DB 2; Length 250;
RESULT 1497
ID AAR05421 standard; protein; 250 AA.
DE Human adipisin/D encoded by a cDNA.
PN WO9001540-A.
PD 22-FEB-1990.
PA (CALB ) CALIF BIOTECHN INC.
Query Match
Best Local Similarity 27.8%; Score 382; DB 2; Length 250;
RESULT 1498
ID ADE58221 standard; protein; 263 AA.
DE Rat Protein AAB31922, SEQ ID NO 4092.
PN WO2003016475-A2.

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PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 27.7%; Score 381; DB 7; Length 263;
RESULT 1499
ID ADN99596 standard; protein; 187 AA.
DE Novel human protein sequence #412.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE ) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 27.6%; Score 379.5; DB 8; Length 187;
RESULT 1500
ID ABU92049 standard; protein; 220 AA.
DE Human protein modification and maintenance molecule-29 (PMM-29).
PN WO2003031939-A2.
PD 17-APR-2003.
PA (INCY ) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 27.6%; Score 379; DB 6; Length 220;

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